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15872 4 05-09-091-0	11.8 15872 3 US-09-109	111	11.8 1626 4 US-09-902	11.8 1344 4 US-09-252	11.8 18331 4 US-09-200 11.8 1200 4 US-09-902	11.8 14158 4 US-09-902	11.8 5001 4 US-09-902	11.8 1224 4 US-09-266	12.0 44377 2 US-08-804	2.2 1998 4 US-09-252	12.2 939 4 US-09-252	12.8 2118 4 US-09-252	12.8 1299 4 US-09-252	13.2 1467 4 US-	15.1 1056 4 US-09-266 15.1 53500 4 US-09-266	Match Length DB ID	Ouery	SUMMARIES	. is the number of results predi- eater than or equal to the score erived by analysis of the total	ISBUAG PATENTE NA.* 1	g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	length: 0 length: 2000000000	f hits satisfying chosen parameters	1202784 seqs, 818138359 residues	Gapop 10.0 , Gapext 1.0	1 atgcgcaacaccggggct	-	April 15, 2005, 17:52:06 ; Search ti	nucleic search, using sw model	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen	
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332 GCATCATCGCCCTAATCCTGGACCGCCGTGACCGCGAAAAGCGGCGCGACCAATCGAG 863 TOGACAACCTCATCGACGAGGGGCGCGCGCATCGACGCTCTTCGTCGACCTGCTG 272 TGGACGAGGAATCGAGCTGGTCCGCCACCGCCAAGCTGGACGACATGAAG 803 TOGTACGCATCCTCCGCCGGATCGCCACCGCCATGAMGCCGGACTCCGGGCTCCTGC 212 cccrcaccachagreracaccccacarancecaccinaccacchaccancccanccara

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ALIGNMENTS	-902-540-5701	US-09-252-991A-3776	US-09-252-991A-3820 US-09-252-991A-3691	US-09-252-991A-5696	US-09-252-991A-5192	US-09-252-991A-5227	US-09-902-540-536	US-09-202-301A-0304	10 00 000 001 306 10 00 000 001 000	US-U9-252-991A-420	US-09-252-991A-373	US-09-103-840A-2	T-W046-501-60-SD	US-08-804-227C-1
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	Sequence 570	Sequence 377 Sequence 358	Sequence 382 Sequence 369	Sequence 689	Sequence 528					Semience 481		compande 373		Sequence 1, A

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9-266-965-06 15.1%; Score 64.4; DB 4; Length 1056;	LENOTH: 1056 ORGANISM: Streptomyces lavendulae	MALIER APPLICATION NAMESCO C. 100-77-77-77 MALIER APPLIANCE APPL 1000 09/133,963 MALIER APPLIANCE THE SENSE OF 100-133,963 MALIER APPLIANCE THE SENSE OF 100-107-107-107-107-107-107-107-107-107-	Punca 66, Application US/09266955 cart No. 649338 cart No. 649338 cart No. 649338 punca 66, Application US/09266955 punca 649338
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923 TCGTCCTCGTCGGCGGCGCCGAACGCTCGGAGAGCGAATTCGCCGCGCGCTGCTGGAGAA

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US-09-902-540-4005
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US-09-266-965-76
SEQ ID NO
                                                                                                                                                                                                                                                         Sequence 4005, Application US/09902540 Patent No. 6833447
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                                 PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                  APPLICANT: Slate; Sieves C.
APPLICANT: Mispand Roger C.
TITUE OF AVENTION: Myxococcus santhus Genome Sequences
FILE REFERENCE: 39-10(18:49): 90-902,540
COMMENT APPLICATION NUMBER: US/09/902,540
COMMENT APPLICATION NUMBER: US/09/902,540
                                                                                                                                                                                           APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
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Best Local Similarity
            NUMBER OF SEQ ID NOS: 16829
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LENGTH: 53500
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EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER FILING DATE: 1996-08-19
EARLIER APPLICATION NUMBER: PCT/US94/1127
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NUMBER OF SEQ ID NOS:
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FILE REFERENCE: 600.456US1
CURRENT APPLICATION NUMBER: US/09/266,965
CURRENT FILING DATE: 1999-03-12
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APPLICANT: Varoglu,
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                                                                                                                                                                                                                                            INFORMATION:
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Pred. No. 0.00017;
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Sequence 1199, Application US/09902540 Patent No. 6833447

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Pred. No. 0.0064;
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US-09-902-540-1199 Matches 178; Conserv Query Match SEQ ID NO 1199 GENERAL INFORMATION: WFULCANT: Alnet, Gregory J.
APPLICANT: Alnet, Seven C.
APPLICANT: Alnet, Seven C.
TITLE OF INVENTION: Wyococcus xanthus Genome Sequences and Uses Thereof
FIRE REFERENCE: 38-10[15849]B NUMBER OF SEQ ID NOS: 16825 PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10 CURRENT APPLICATION NUMBER: US/09/902,540 CURRENT FILING DATE: 2001-07-10 APPLICANT: APPLICANT: Goldman, ORGANISM: Myxococcus xanthus TYPE: DNA 26533 Hinkle, Barry S. 13.2%; Score 56.2; DB 4 Pred. No. 0.0078; DB 4, Length 26533;

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12713 CTGGCCGAGGACGGCACGGCGTTTCCTGGACGAGATTGGCGACATGTCGCTGATGCTCCAG

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163 GACCTOGTTGCCCGGGTCGCCCAGGTGCTCGGCCTCGACCTCGACGAAGCCCTCGCCGCC 222

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US-09-252-991A-5631
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 173; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 198-02-16
PRIOR APPLICATION NUMBER: US 60/094,190
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CURRENT FILING DATE: 1999-02-18.
CURRENT FILING DATE: US 60/074,788
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WERFION: NUCLEIC ACID AND MAINO ACID SEQUENCES RELATING TO PSEUDOMONAS
WYEMFION: ARRUGINOSA FOR DINGNOSTICS AND THERAPBUTICS
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Pred. No. 0.015;
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US-09-252-991A-5600
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SEQ ID NO 5600
LENGTH: 1611
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PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ARRICATIONS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5605, Application US/09252991A
Patent No. 6551795
GENERAL INCORMATION:
APPLICANT: Marc J. Rubenfield et al.
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LENGTH: 2118
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CURRENT FILING DATE: 1999-02-18
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PRIOR FILING DATE: 1998-07-27
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PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                          TYPE: DNA
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
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pred. No. 0.015;
Score 54.4; DB
Pred. No. 0.015;
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Length 1611;

Indels

Gap

Query Match

SEQ ID NO 5631

APPLICANT:

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627 303 567 243 510 183

RESULT 6 US-09-252-991A-5600/c

Best Local Similarity Query Match

12.8%;

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687

Matches

173; Conservative

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PRIOR PELICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 345
LENGTH: 939 GENERAL INFORMATION: Sequence 3645, Application US/09252991A Patent No. 6551795 APPLICANT, MART G. RUBERISCH de al.
APPLICANT, MART G. RUBERISCH de al.
TITLE G. EMPRITCH, MUTLER ACED AND ANTO ACID SUQUENCES RELATING TO BENDOCCOMA
TITLE SEFENCE, 107156 SERVICON DE DIAMOSTICS AND THERAPEUTICS
CHEERED FERENCE, 107156 SERVICON DE DIAMOS 09-252-991A-3645 TYPE: DNA ORGANISM: Pseudomonas aeruginosa Local Similarity 254 528 194 468 408 134 Адалсаасалалассаасссалсалсанстванстваттассавстваестрастра 348 194; 862 CGAGGCCAAGGTGCCGGTGATCAAGCACCTGGACGGCATCTGCCACGTCTAC 913 363 GCGCGACAAGGCGGCGGCGATCGAGGCAAACCAAGGGGCTCATCGACCTGTTC 414 303 243 CACCCCGCCAGCGACCCCAACCATGGACCTGGACGAGGAAATCGAGCTGGTCCGCACCGA 302 183 625 GTGCCTGAAGTCCGGCAACGCGACCATCCTGCGCGGGGGGCTCCGAGGCGATCCACTCCAA 123 соессеятеленасиссия для принцента принцент GGGTČAČCTAČÁGCĠGĊGAĠĠAĊĠĀAĊTGGCGCĀAĊTĠĠGĊGAGCGĊTTĊAAĊCAĞAŤĠĠ 647 семсуссим сситеемсствей семеним тесмествету сесместем зта TGTTCCTCAGCCTGCTGGTGGTGTTCGTCACCCTCTACGACCTCAGCTATCACGTCATCG TCCTCCAGGCCAAGGCCGAAGCGCCGCCGCTCGCAACTGCTCAGCACGGTGCAGGGCCTGTGCCC 467 TGACCANGAGCGAGTTGGCCAGGGGATCCAGAAGGACCGGGGCACCGTCGGCCGGTGGG 133 COCTGCCCGGACGCGCTGCTGGACGCCTACGTCGGCGACATCGACCCTTTCGTCGGCA 407 CGAATÁCGTCGÁČGTGATCGTCCCGCGCGCGGGGAAGGGCCTGÁTCGAGCGCATCAGCCG 861 ссссья в стора с сва с в правети в п CGCCGTGCAGGTGGTAAACCACCGACCGCGCGCGCGGTCGGCGCGCTGATCAGCATGCC COMEGCEATCECCCCCCCCCATCCMGCAGGGCCTGGCCGAGGCCGGCCTG--CCAGGTGCTCGACCTCGACGAGGAGGAAGCCCTCGCCGCGGAGGTCTGCGCCCCGGGGT 242 GGGCGTGGTCGGGATCATCTACGÁGTCGCGGGCCGAACGTGACCÁTCGÁCGCCGCCÁGCCT GCGCGCCGGACTGACCAAGAGCGAGTTGGCCAGGCGCATCCAGAAGGACCGGGCCACCGT Conservative 12.2%; Pred. No. 0.045; 0; Mismatches 210; Score 52; DB 4; Length 939 Pred. No. 0.045; 0, Mismatches 176; Indels Indels 6 ω, Gaps 527 801 684 624 S 밁 Ş 밁 Q Bb ą 밁 S 멍 Ś 밁 GENERAL INFORMATION: APRICANT: MACS RUMENTED Et al.
TITHE OF IMPRICA. MOUSECACID AND AMENO ACID SEQUENCES RELATING TO PREUDOMONAS
FILE REFERENCE: 10118-136
FILE REFERENCE: 10118-136 S

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RESULT 10 US-09-252-991A-3812/c Sequence 3812, Application US/09252991A Patent No. 6551795 US-09-252-991A-3697 US-09-252-991A-3697 믕 S 밁 Matches 194; Sest Local CURRENT PAPLICATION INVESES: US/0752,991A
CURRENT FILING NATE: 1959-0-186/074,788
PRICER APPLICATION INVESES: US 60/074,788
PRICER FILING NATE: 1959-0-196/074,788
PRICER APPLICATION INVESES: US 50/094,190
PRICER FILING NATE: 1958-0-79
RECER FILING GENERAL INFORMATION: Sequence 3697, Application US/09252991; Patent No. 6551795 ORGANISM: Pseudomonas aeruginos: FILE REFERENCE: TITLE OF INVENTION: APPLICANT: Marc J. TYPE: DNA LENGTH: 1881 773 374 719 314 ACGAGGACATGAAGCGGCGCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGCGACAAGG 373 659 599 194 GCCTCGACCTCGACGAAGCCCTCGCCGCCGCCGCGCCCCGGCCCCCGCCGCCACCCCGCCAG 253 539 TGTTCCTCAGCCTGCTGGTGGTGTTCGTCAGCCTCTAGGACCTCAGCTATCACGTCATCG 134 AGGAÇGGÇAAGAACÇGGCCCGACGACGACGGACCTCGTTGCCCGGCGTCGCCCAGGTGCTCG 193 419 CÓCTÓCCCGGACGCGCGCTGCTGGACGCCTACGTCGGCGACATCGACCGTTTCGTCGGCA 478 74 14 севбественасоснатання подсержиться температосная подсержения та 374 64B CCGGCGAGCTGAAGAG 314 ACGAGGACATGAAGCGGCGCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGCGACAAGG 373 CCCGCGCCCTCTCGCAGAGCCACCAGCGTCGTACGTCTACGCCAGC 822 CGGCGGCGATCGAGGAAACCAAGCGGCTCATCGACCTGTTCCGGCGGAGC 423 CCGGCGAGCTGAAGAG GGGTCACCTACAGCGGCGAGGACGAACTGGCGCAACTGGGCGAGCGCTTCAACCAGATGG GCCCGCTGCGCGAACTCACCAGCACCSCCCGCCGCCGCGCGGCGGCGAGCTGGACGCGC 658 Similarity TOCTECHÁGECCHAGGECGAGCGCGCTCGCHACTGCTCAGCACGGTGCAGGGCCTGTGCC 538 TGACCAMGAGCGAGTTGGCCAGGCGCATCCAGAMGGACCGGGCCACCGTCGGCCGGTGGG 133 CCCGCGCCTCTCGCAGAGCCACCAGCCTCGAACTGCTCACGCCAGC CGGCGGCGATCGAGGAAACCAAGCGGCTCATCGACCTGTTCCGCCGGAGC 423 Conservative 107196.136 Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS 12.2%; Score 52; DB 4; Length 1881; 47.3%; Pred. No. 0.047; -CATCIACGGCGACCTGGAAGAGCGCGTGGAGGACAAGA 772 Mismatches -CATCTACGGCGACCTGGAAGAGCGCGTGGAGGACAAGA 701 210; AND THERAPEUTICS Indels 6, Gaps TO PSEUDOMONAS 598

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US-09-252-991A-3812
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LENGTH: 1998
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Patent No. 5876991
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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MEDIUM TYPE: Floppy
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                                                                                                                        CURRENT APPLICATION DATA:
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PLICANT: Rosteck, Paul R., Jr.
PLICANT: Suction, Kimberly L.
TLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                             OPERATING SYSTEM:
SOFTWARE: ASCI(DO
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FILING DATE:
                                                APPLICATION NUMBER: US/08/804,227C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 ACCAGGACATGAAGCGGCGCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGCGACAAGG 373
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IBM Compatible
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Pred. No.
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Patent No. 5945320
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                         APPLICANT: ROSTECK, Paul R.; Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25949 CCGAGGGGCGGCGGGGGGGGTTCTCCTCGTTCGGCATCAGCGGCACCAACGCGC
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ADDRESSEE: PAUL R. CANTRELL
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5945320
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0; Gap

CLASSIFICATION:

Rao, Nagaraja R. Richardson, Mark A.

1138

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US-08-804-227C-7
             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                   NAME: Plant, Thomas, G.
REGISTATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                            MOLECULE TYPE:
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nucleic acid
Conservative
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                                                                 36155..41830
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                                                                                                                                              20110..31284
                                                                                                                                                                                                                                                                  DNA (genomic
               47.9%;
                                                                                                                                                                                                                                                                                                                                                                                      X-8231
     0; Mismatches 160;
                  Score 51;
Pred. No.
                     0.094;
                                  DB 2;
                                  Length 44377;
          Indels
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LILLY CORPORATE CENTER

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US-08-804-198-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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26249 TCGAGCA 26255
                                                                                                                26189 CCCACCCGGAGCTGCÁCCCGGCCGÁCGTCGGCTÁCACCCTCATCÁCCACCCGCÁCCCGGT 26248
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                                                                                                                                                                                                                                                                                                                                                                                                            26069 COGACGGCGACGTCTCGTCCGAGGAGTGGTGGCACGAGGTGACCGTGCCCCCTGATGATGT 26128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25949 CodnágodocododocododostenTerecrocorridadenTendocodenConacidodenCo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26009 TCGTCATCGAGGAĞCCGCCGGAĞCCCACCGCCGAACTGCTCGCGCCCGAACCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: LALL.
CITY: INDIANAPOLIS
                                                                          314 ACGAGGA 320
                                                                                                                                                                                           254 СБАССССААССАТОВАССТОВАСОВАФВААЛТСВАОСТВОТСОВСАССОВАССССАЛОСТВО 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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350..14002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 2; Length 44377;
Pred. No. 0.094;
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APELCONT: MIATHA GROUP J.
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APELCONT: Slates, Seven C.
APELCONT: ABSOLUTION SANCTION SANCTION CONTROL OF THE SEVEN APPROXIMATION SANCTION SANCTION CONTROL OF THE SEVEN APPLICATION SANCTION SANCTION CONTROL PRICES DATE: MOMERIC US 09/902, 540
BRICE APPLICATION SANCTION CONTROL OF THE SEVEN APPLICATION SANCTION SANCTION

Genome Sequences and Uses Thereof

PRIOR APPLICATION NUMBER: 60/217,883

2000-07-10

NUMBER OF SEC ID NOS: 1682 PRIOR FILING DATE: GENERAL INFORMATION: APPLICANT: Goldman, APPLICANT: Hinkle,

Sequence 8618, Application US/09902540

Patent No. 6833447

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US-09-902-540-8618
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US-09-266-965-22
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Best Local Similarity 47.5%; Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BARLIER FILING DATE: 1993-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: US 08/133,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER FILING DATE: 1996-08-19
EARLIER APPLICATION NUMBER: DCT/US94/11279
EARLIER FILING DATE: 1994-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
FILE REFERENCE: 600.465U81
CURRENT APPLICATION NUMBER: US/09/266,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: He, M
APPLICANT: Sheldon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Varoglu, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sherman, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 1224
                                                                                                                                                                                                 1161 GCGCGACGACCAGATC 1176
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                                                                                                                                                                                                                                                                                                  399 GCTCATOGACCTGTTC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 СОСССТЛАТССТВЕМЕСЕССЕТВАБСЕСБАБЛАБЕСЕВЕСЕВЕСЕВТСЕМЕСЬАВСЕ 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 GGAAATCGAGGTGGTCCGCACCGACCCCAAGCTGGACGAGGACATGAAGCGGCCCATCAT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  981 CCCCGACCCGACCGCCTCGACATCACGCGCGAGCACAACCCCGCACCTCGGCCTTCGGCCA 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 свессвенаем стверене в предоставления предостав
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               921 GANGACÓGGGGAGTÖÖTTGETGGÖÖTTGGCTGGCGGCGANGCGGGGNCCCGGCGGTÖTT 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 GGCGGACCTCGTTGCCCGCGTCGCCCAGGTGCTCGGCCTCGACGACGAAGCCCTCGC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 САТССАGAAGGACCGGGCCACCGTCGGCCGGTGGGAGGACGGCAAGAACCGGCCCGACGA 158
                                                                                                                                                                                                                                                                                                                                                                              6495348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1224;
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8395 CÓGCÁTCCACCTCTGCCTGGGCATGGAGCTCGCCCGGGTGGAGATGGGCCAGGCGTGG 8335 CCCCGACCCCGACCCTCGACATCACGCGCGAGCACAACCCGCCACCTCGCCTTCGGC

279 GGAMATCGMGCTGGTCCGCACCGACCCCAMGCTGGACGACGACATGAAGCGGCGCATC

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LENGTH: 5001
TYPE: DNA
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                                                        US-09-266-965-74
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GENERAL INFORMATION:
                                    Sequence 74, Application US/09266965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2591 TOGCCCTGCOGCTGTCCGCCGCGGTGGACTTGGACAAGAGCCCCCGCCGAGGCACGCTGG 2650
                                                                                                                                                                                                                      2771 TágCATCCGCGCAGGÁCGCGGÁCGAGGCCCTGGAGATGCTGCTGCGCACCGCCGAGCTGG 2830
                                                                                                                                                                                                                                                                                                   2711 AGCGAÓGCCTGCGGCÁGGCGGGTGACGCCGCGGGGGCTGGGCGCCTGTACÁCCATGCGGC 2770
                                                                                                                                                                                                                                                                                                                                                                                    2651
                                                                                                                                         2831 CGGA 2834
                                                                                                                                                                                                                                                                                                                                           194 GCCTCGACCTCGACGAAGCCCTCGCCGCCGCCAGTCTGCGCCCCGGCGTCACCCCGCCAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                        134 AGGACGGCAAGAACCGGCCGAACGACGCGGACCTCGTTGCCCGCGTGGCCAGGTGCTCG 193
                                                                                                                                                                              314 ACGA 317
                                                                                                                                                                                                                                                          254 салссосласситерассторасварамлятоваестретсовелесоваесселастве 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 ТОЛССАЛОЛОСЬЛОТТООССЛООСОСТССАВЛАСОЛССООССЛОСТСООССООТООС 133
                    6495348
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; TYPE: DNA ; ORGANISM: Streptomyces lavendulae US-09-266-965-74

Matches Query Match

Local Similarity hes 150; Conserv

Conservative

0; Mismatches 166; Indels Score 50.4; DB 4; Length 12249; Pred. No. 0.11;

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SOFTWARE: FastSEQ for Windows Version 3.0 EARLIER APPLICATION NUMBER: US 08/133,963 EARLIER FILING DATE: 1993-10-07 BARLIER FILING DATE: 1994-10-06 EARLIER APPLICATION NUMBER: US 08/624,447 TITLE OF INVENTION: Mitomycin biosynthetic gene cluster FILE REFERENCE: 600.456US1
CURRENT APLICATION UNMERS: US/09/266,965
CURRENT FILING DATE: 1999-03-12

APPLICATION NUMBER: PCT/US94/11279

E: 1996-08-19

NUMBER OF SEQ ID NOS: LENGIH:

APPLICANT: Varoglu, M. APPLICANT: He, M. APPLICANT: Sheldon, P.

APPLICANT

Job time : 96.1904 secs Search completed: April 15, 2005, 19:15:57

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8204.076 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 54677, A
Sequence 73639, A
Sequence 73639, A
Sequence 3520, Ap
Sequence 4348, Ap
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Sequence 2, Application US/09855340 Patent No. US20020076788A1

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	•	6; Conservative 0;	100.0%;	G-09-855-340-2	TYPE: DNA	SEQ ID NO 2	SOFTWARE: Patentin Ver. 2.1	NIMBER OF SEO ID NOS: 9	DRIOR FILING DATE: 2000-05-17	CURRENT FILING DATE: 2001-05-15	CURRENT APPLICATION NUMBER: US/09/855,340	PILE REFERENCE: IN01164K	TITLE OF INVENTION: halophitics and Micromonospora carbonacea chrome	TITLE OF INVENTION: Site-specific integration into Micromonospora	TITLE OF INVENTION: ISOISCION OF PROCEEDING FUNCTION	APPLICANT: Horan, Ann C.	APPLICANT: Hosted, Jr., Thomas J.	OBNIBOR INCOMPLICATION
	Db 1 ATGOSCAACACACCGGGGCTGGGGGGGCACATGGGCCGCATACGTCCTCACGGC	Gy 1 ATGGGANENERGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Best Local Matches 4	Query Mato Best Local Matches 4	ORGANISM -09-855-34 Query Matc Best Local Matches 4	TYPE: DN ORGANISM -09-855-34 Query Matc Best Local Matches 4	SEQ ID NO TENGTH: TYPE? DN ORGANISM ORG	SOFTWARE: SOFTWARE: DROID NO SEQ ID	NUMBER OF SOPTWARE: SOPTWARE: DEO ID NO LENGTH: TYPE: DN ORGANISM -09-855-34 Query Matc Deet Local Matches	PRIOR FIL PRIOR FIL PRIOR FIL PRIOR FIL SO TIME: SEQ TIME: LENGTH: TYPE: DN ORGANISM ORGANISM OLGEN MATG OLGEN MATG Deet Local	CURRENT F PRIOR APP PRIOR FIL NUMBER FOR SOPTWARE: SEQ ID NO LENGTH: TYPE: DN ORGANISM -09-855-34 Query Matc Best Local Matches 4	CURRENT A CURRENT F PRIOR APP PRIOR FIL NUMBER OF SOPTWARE: SOPTWARE: DE SOPTWARE: TYPE: DN ORGANISM OP-855-34 Ouery Matc Guery Matc Gest Local Matches			TITLE OF TIT			

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APPLICANT: Sherman, David. H
APPLICANT: Mac, Yingqing
APPLICANT: Warcoglu, Mustafa
APPLICANT: He, Min
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Publication No. US20030134398A1
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PRIOR APPLICATION NUMBER: 09/266965
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PRIOR APPLICATION NUMBER: PCT/US00/06394
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CURRENT FILING DATE: 2001-09-12
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APPLICANT: Sheldon, Paul
TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
FILE REFERENCE: 600.530US1
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ORGANISM: Streptomyces lavendulae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCACCCCCCACCAACCATGGACCTGGACGAGGAAATCGAGCTGGTCCGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCAGGTGCTCGGCCTCGACCTCGACGAAGCCCTCGCCGCAGGTCTGCGCCCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64.4; DB 10; Length 1056;
Pred. No. 5.5e-07;
0; Mismatches 146; Indels 0;
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                                                                                                                                                                                                                                                                                                           Sequence 76, Application US/09953348
Publication No. US20030134398A1
REPLICANT: He, Min
APPLICANT: Sheldon, Paul
TITHE OF INVENTION: MITOWYCIN BIOSYNTHETIC GENE CLUSTER
FILE REPERBYCE: 600.530US1
                                                                                                                               APPLICANT:
                                                                                                                                                                                           APPLICANT: Sherman, David. H
APPLICANT: Mao, Yingqing
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RESULT 4
US-09-953-348-76
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LENGTH: 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/133,963
PRIOR PILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 08/624,447
PRIOR PILING DATE: 1996-08-19
PRIOR APPLICATION NUMBER: PCT/US94/11279
PRIOR FILING DATE: 1994-10-06
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CURRENT FILING DATE: 2002-10-09
FRIOR APPLICATION NUMBER: US 09/266,965
PRIOR FILING DATE: 1999-03-12
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APPLICANT: He, M
APPLICANT: Sheldon, P
TITUS OF INVENTION: Mitomycin biosynthetic gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 600.456US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sherman, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptomyces lavendulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        803
                                                                                                                                                                           923 TCGTCCTCGTCGGGGGGGCCGAACGCTCGGAGAGCGAATTCGCCGCGCTGCTGGAGAA 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         743 CCGACGGCCCGACGTCTACCTCATCAAGCACGTGCTGCACGACTGGGACGACGACGACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        683 CCGGCCGCGGCTCGCGGACCGGTGCGAGATCCTGCCCGGCGACTTCTTCGAGACCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOGTACGCATCCTCCGCCGGATCGCCACCGCCATGAAGCCGGACTCCCGGCTCCTGGTCA 862
                                                                                                                                                                                                                                                                     GEATCATCGCCCTAATCCTGGAGCGCCGTGAGCGACAAGGCGGCGGCGATCGAGGA 389
                                                                                                                                                                                                                                                                                                                                                                TCGACAACCTCATCGACGAGCGGCCCGCGGCATCGACGCTCTTCGTCGACCTGCTGCTGC 922
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Pred. No. 5.5e-07;
0; Mismatches 146;
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CURRENT APPLICATION

NUMBER: US/09/953,348

Varoglu, Mustafa

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US-10-267-255-76
                                                                                                                                   TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-10-267-255-76
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SEQ ID NO 76
LENGTH: 53500
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Publication No. US20030124689A1
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                                          Matches 152;
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                        SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptomyces lavendulae
-09-953-348-76
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PRIOR REPLICATION NUMBER: US 09/266,965
PRIOR FILING DATE: 1999-03-12
PRIOR REPLICATION NUMBER: US 08/624,447
PRIOR FILING DATE: 1996-08-19
PRIOR REPLICATION NUMBER: ECT/US94/11279
PRIOR FILING DATE: 1997-10-06
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PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/266965
                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/267,255
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                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1993-10-07
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 08/133,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 600.456US1
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TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
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                                                                                                                                                                                                     ENGTH: 53500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43636 TOGTACGCATCCTCCGCCGGATCGCCACCATGAAGCCGGACTCCCGGCTCCTGGTCA 43699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 CCCTCGCCGCAGGTCTGCGCCCCGGCGTCACCCGCCAGCGAGCCCCAACCATGGACC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 CCAGGCGCATCCAGAAGGACCGGGCCACCGTCGGCCGGTGGGAGGACGGCAAGAACCGGC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGCGACAAGGCGGCGGCGATCGAGGA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGACAACCTCATCGACGAGGGGCCGGCGCATCGACGCTCTTCGTCGACCTGCTGCTGC 43759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGACGAGGAAATCGAGCTGGTCCGCACCGACCCCAAGCTGGACGAGGACATGAAGCGGC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGACGGCCGACGTCTACCTCATCAAGCACGTGCTGCACGACTGGGACGACGACGACGACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COGACGACGCGGACCTCGTTGCCCGCGTCGCCCAGGTGCTCGGCCTCGACCTCGACGAAG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Varogiu, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mao,
                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.1%;
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                                                             15.14;
                                                                                                                                                                                                                                                    Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 64.4; DB 10;
Pred. No. 3.4e-07;
0; Mismatches 146;
                                                             Pred. No. 3.4e-07;
                                          Mismatches
                                          146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 53500;
                                          Indels
                                                                                    Length 53500;
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US-10-425-115-73639/c
Sequence 73639, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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                                                                                         RESULT 7
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SEQ ID NO 54677
LENGTH: 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 54677, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT4530_56759C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43756 TCGTCCTCGTCGGCGGCGGCGAACGCTCGGAGAGCGAATTCGCCGCGCTGCTGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43636 TEGTACGEATECTCCGCCGGATCGCCACCGCCATGAAGCCGGACTCCCGGCTCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43516 CCGGCGGGGCTCGCGGACCGGTGCGAGATCCTGCCCGGCGACTTCTTCGAGACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 AGGAMATCGAGCTGGTCCGCACCGACCCCAAGCTGGA 314
                                                                                                                                                                                                                                                    158 ACCCCGACCTCGTTGCCCGCGTCGCCCAGGTGCTCGGCCTCGACCTCGACGAAGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                       399 GCAGCCAGAGCTACGTGCTCACCAAGGGCTGGAGCCGCTACGTCAAGGAGAAGCGCCT
                                                                                                                                                                579 CÓCCGCAGCCÓCCTGCCCTCAACGGCGGCGAGCAGCA 615
                                                                                                                                                                                                                                                                                               218 CCGCCGCAGGTCTGCGCCCCGGCGTCACCCCGCCAGCGACCCCAACCATGGACCTGGA
                                                                                                                                                                                                                                                                                                                                              459 ACGCCGGCGACGTCCACTTCGAGCGCGTCCGCCGCCTCGGCGCCGCCGACCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 GCATCCAGAAGGACCGGGCCACCGTCGGCCGGTGGGAAGGACGGCAAGAACCGGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kovalic, David K.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOGACAACCTCATCGACGAGCGGCCGCGCGCATCGACGCTCTTCGTCGACCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOGACGAGGAMATCGAGCTGGTCCGCACCGACCCCAAGCTGGACGACGACATGAAGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGACGACGCGACCTCGTTGCCCGCGTGGCCCAGGTGCTCGGCCTCGACCTCGACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boukharov, Andrey A
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 63.4; DB 18;
Pred. No. 9.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1033;
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<u>.</u>; Gap

92 CCAGGCGCATCCAGAAGGACCGGGCCACCGTCGGCCGGTGGGAGGACGGCAAGAACCGGC 151

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US-10-425-114-25190
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                                                                                                                                                                                                                                                                                                  APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Stoven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
    Query Match
                                                                                                                                         SEQ ID NO 25190
LENGTH: 2129
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25190, Application US/10425114
Publication No. US20040034888A1
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LENGTH: 683
                                                                                                                                                                                                              APPLICANT: (de, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE, 1921(5311)18

CHERRY PRICEOTION NUMBER: US/10/425,114
                                                                                                                                                                             CURRENT FILING DATE: 2003-
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -10-425-115-73639
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CURRENT APPLICATION NUMBER: US/10/425,115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
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APPLICANT: Cao, Yongwei
                                                                                PEATURE:
                                                                                                ORGANISM: Zea maye
                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: MRT4577_167158C.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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LOCATION: (1)...(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 AGCTGGTCCGCACCGACCCCAAGCTGGACGAGGAC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 GTCTGCGCCCCGGCGTCACCCCGCCAGCGACCCAACCATGGACCTGGACGAGGAAATCG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 TCGTTGCCCGCGTCGCCCAGGTGCTCGGCCTCGACGAAGCCCTCGCCGCCGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 ACGGTGCCGGCCTCGAGGTCCACCTTGGCGAAGCC 46
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                                                        Clone ID: LIB3732-006-E3_FL3
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    14.24;
    Score 60.6; DB 17;
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Pred. No. 5.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134;
Length 2129
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378 318 156

216 CGCCGCCGCAGGTCTGCGCCCCGGCGTCACCCCCGCCAGCGACCCCAACCATGGACCTGGA 275

CGACCTCCCGCTTCCCGCTACCTGGGCGGCCCGAACGCGCACCTGCTGCCCGTTCCGAT

258 GCAGCGCCTGATCGACCAGGCGATGTTCGACCTGGACGCCCACCGACAACAAGGGCTCGCT

317

377

CGACGCGGACCTCGTTGCCCGGGTCGCCCAGGTGCTCGGCCTCGACCTCGACGAAGCCCT 215 GCGCATCCAGAAGGACCGGGCCACCGTCGGCCGGTGGGAGGACGGCAAGAACCGGCCCGA 155

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US-10-156-761-3520
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                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3520
LENGTH: 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                            Matches
                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3520, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ISHIKAMA, UIN
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: SHEMA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 51.3%;
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                      LENGTH: 12
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REPERENCE: 249-262
                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1724
    198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AGGACCGGGCCACCGTCGGCCGGTGGGGAGGACGGCCAAGAACCGGGCCGACGACGACGCGACC 166
                                                                                        154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47
                                                36 GGCCGCATACGTCCTCACCGCCGCGGGGGCGCCGGACTGACCAAGAGCGAGTTGGCCAG 95
                                                                                                              l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141; Conservative
GGCCGTCCTCGCCGTCATCGAGCAGATCGGCCCGGAGCTCGTCGGCTACGACGCCACCGA
                                                                                                                                                                                                       £ 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTGCGCCCCGGCGTCACCCCGGCCAGCGACCCCATGGACCTGGACGAGGAAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGGCCTCGGCCCGCATGTCGCGGGGCGTTGACGACGACGACTTTCCGACGCGCCGCGGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCTGGTCCGCACCGACCCCAAGCTGGACGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOGITGCCCGGGTCGCCAGGTCCTCGGCCTCGACCAAGCCCTCGCCGCCGCAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTCACCGCCGCGAGGCGCGGACTGACCAAGAGCGAGTTGGCCAGGCGCATCCAGA 106
                                                                                        Conservative
                                                                                                              13.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                    Score 58.6; DB 15
Pred. No. 1.5e-05;
0; Mismatches 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 134;
                                                                                                                                DB 15;
                                                                                        159,
                                                                                        Indels
                                                                                                                                Length 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                        0
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    257
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41 -1

RESULT 11 US-10-155-61-1 Sequence 1. Application US/10159761 Publication No. US2003011901801	Oy 338 TCCCC 342. Db 1205 TCCCC 1209	Oy 278 AGRANATCHACTOCONCONCONCONCONTONAGACATON	оу 218 совосказартителенскоговогомостическогомост	Qy 158 AcadeaAccretinecrosorreaccosenterrosecritaAccretia 217 In 1 1 1 1 1 1 1 1 1 1	Oy 98 GENTICHIGANGARCOGGECACCTGGECGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	Db 905 CCCATROSTICTION-COCCOCCAGGIOCICCAGARTIACCAGATICACCAGTICACCAGT Db 905 CCACCOTCGACATGGGCCCCGCGAGGTCGTACGGCTCGACCAGGTCCACCTGGGCTTCG 964	Query March 13.8t; Score 58.6, DB 15; Løngth 1365; Best Local Similarity 49.5t; Fred. No. 1.58-05; Matches 151; Conservative 0; Mismatches 154, Indels 0; Gaps 0;	I NAME/KEY: C19: I LOCKTON: (1): (1365) US-10-156-761-4348	ORGANISM: Streptomyces avermitilis FEATURE:	NUMBER OF SEQ ID NOS: 15109 SEQ ID NO 4348 LENGTH: 1155	PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FLING DATE: 0001-05-30 PRIOR FLING ANTE: 0001-05-30 PRIOR PAPLICATION NUMBER: JP 2001-272697 PRIOR FLING DATE: 0001-08-02	FILE REPERENCE: 120 MBER: US/10/156,761 CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT PILING DATE: 2002-05-29	APPLICANT: SAKAT, YOSHITUKI APPLICANT: SAKAT, YOSHITUKI APPLICANT: HATTORI, MASAHITA TITSE OR THUBETUKI, MASAHITA TITSE OR THUBETUKI		GENERAL INFOGMATION: APPLICANT: OWURA, SATOSHI APPLICANT: AVENDA HARUO	U8-10-156-761-4348 ; Sequence 4348, Application US/10156761 ; Publication No. US20030119018A1	RESULT 10	Oy 336 CATCOCCCTANTC 348	Oy 276 COMMANDEMACTICAL CONTROL COMMAND AND AND AND AND AND AND AND AND AND
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PILE REPRINCE: 202 262 PILE REPRINCE: 100 262 CORRENT APPLICATION NOMER: US/10/156,761 CORRENT PILMS DATE: 2002-05-29 PRIOR APPLICATION NOMER: JP 2001-204089	APPLICANT SIZE AWAY A NOSIUA APPLICANT SIZE AWAY NOSIUA APPLICANT SIZE NOSI NOSI APPLICANT SIZE AWAY NOSI AND APPLICANT SIZE NOSI NOSI NOSI NOSI NOSI NOSI NOSI NOSI	GENERAL INFORMATION: APPLICANT: OWURA, SATOSHI APPLICANT: IKEDA, HARUD APPLICANT: IKEDA, HARUD APPLICANT: ISHIKAWA, JUN APPLICANT: USHIKAWA, JUN	RESULT 12 US-10-156-761-1/c Sequence 1. Application US/10156761 Publication No. US20030119018A1	Db 5343191 TCCCC 5343195	5343131	Db 5343071 ἀλακτικό το καιτολοκοί το προστορικό της της το προστορικό της	pb \$3,43,011 содырственностиностиностиностиностиностиностиност	pb 5342951 ccececidas/ccda/aceasac/fromostrocearace/coa/aceasac/fromostrocearace/coa/aceasac/fromostrocearace/coa/aceasac/fromostrocearace/coa/aceasac/fromostrocearace/coa/aceasac/fromostrocearace/coa/aceasace/coa/aceasace/c	QY 98 GCATCCAGAAGGACCGGGCCACCGTCGGCCGGTGGGAGGACGCCAAGAACCGGCCCGA	Oy 38 CCCATACOTCCACACACCCCCCACACCCCCCCACACCCACC	Query Match 13.8%; Score 58.6, DB 15; Les Best Local Similarity 49.5%; Pred, No. 5.3e-06; Matches 151; Conservative 0; Mismatches 154; Inc.	t, c, g, other or unknown	ORGANISM: Streptomyces avermitials FENTURE: NAME/KEY: misc_feature	LENGTH: 9025608 TYPE: DNA	PRIOR FILING DATE: 2001-08-02 PRIOR FILING DATE: 2001-08-02 NUMBER OF SEQ ID NOS: 15109	PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30 PRIOR FILING DATE: 2001-05-30	FILE REFERENCE: 249-262 CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29	APPLICANT: SAKAKI, YOSHIYUKI APPLICANT: HATTORI, MASAHIRA TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES	APPLICANT: IKEBA, HARUO APPLICANT: IKEKAMA, JUN APPLICANT: HORIKAMA, HIROSHI APPLICANT: SHEBA, TÄDÄYÖSHI
					TGGGCGTCGGCCGCAT	ncggggfgttcggcgt ncatgaagcggcgcat	DOGGACCGGCACCCT	ACGCGCACGCGCGGA WCCTCGACGAAGCCCT	GCAAGAACCGGCCCGA	AGAGCGAGTTGGCCAG	Length 9025608; indels 0; Gap				X				0

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; GENERAL INFORMATION:
IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
                                                   OMURA, SATOSHI
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Query Match Best Local Similarity

13.6%; Score 58; DB 15; 48.8%; Pred. No. 2.1e-05

Length 1332

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US-10-156-761-4084
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US-10-156-761-4084
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                                                                                                        SEQ ID NO 4084
LENGTH: 1332
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4084, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                          NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                         PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                     APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 154,
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                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                  LOCATION: (1)
                                     NAME/KBY: CDS
                                                        FEATURE:
                                                               ORGANISM: Streptomyces avermitilis
                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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LOCATION: (4187715)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 9025608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4373341 GGCCGTCCTCGCCGTCATCGAGCAGATCGGCCGGAGCTCGTCGGCTACGACGCCACCGA 4373282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 CATCGCCCTAATC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L GATGAACATCCTGAACGGCGGCTCGCACGCCGACTCCAACGTGGACATCCAGGAGTTCAT 437304:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAGGAAATCGAGCTGGTCCGCACCGACCCAAGCTGGACGACATGAAGCACGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACCTCCCGCTCTTCCGCTACCTGGGCGGCGCCCGAACCCTGCTGCCCGTTCCGAT 4373102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCGCCGCAGGTCTGCGCCCGGCGTCACCCCGCCAGCGACCCCAACCATOGACCTGGA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGACGCGGACCTCGTTGCCGGCGTCGCCCAGGTGCTCGGCCTCGACCTAGGCCCT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGGGCCTGATCGACCAGGCGATGTTCGACCTGGACGACCACCGACAACAACAACAACGGCTCGCT 4373222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCGCCAACGCCATCCTCGGCGTCTCCCCTCGGCGTCGCGCACGCCGCCTCCGAGGCCAG 437316;
                                                                                                                                                                                                                                                                                                                             SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                        LKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           SATOSHI
                                                                                                                                                                                                                                2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.3e-06
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; FEATURE:
; CTHER IMPORMATION: Clone ID: PAT_MRT4530_75212C.1
US-10-437-963-75092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 75092
Matches
                                                   1898
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRUICANT: 11, Ping
INTEL OF INVENTION: sice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1108
                                        y Match 13.6%;
Local Similarity 47.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 GGACCTCGTTGCCCGGGCTCGCCCAAGGTGCTCGACCTCGACGAAGGCCTCGCCGC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          780 CAAGAACCTCTGGGGGCACGTCCGCCGCTGGGGGGATCATGATCGCCGTCATCCTCGT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 ссланиванская селествення праводня 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCATCATGCAGGGCGCCGAGGGCAAGGCCGCCGCGATCATCAGCTCCCCGGCGACCCT
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Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boukharov, Andrey A.
Barbazuk, Brad
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                              Score 57.8, DB 18;
Pred. No. 2.4e-05;
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                                                                       Length 1108;
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225 AGGTCTGCGCCCCGGCGTCACCCCCCCCCCCCACCCATGGACCTGGACGAGGAAAT 284 792 GCTCGGCCCTGGCGACGTACACGCGGTGCGACGTCACGGACGACGACGCACGTCGCCGC 852 TGGCGCCAAGGTTATACTCGCCGACGTCCAGGACCTCGGCCGCCGCCGCCGCCGCCGA

733 224 793 164 85

912 CGTCATCACCGGCGCCGCCAGCGGCATCGGCAAGGCGTCGGCGAAGGAGTTCATCGGCAA

45 CGTCCTCACCGCGCGCGCGCGCGCGCGCGCTCCAAGAGCGAGTTGGCCAGGCGCATCCA

Mismatches

202;

Indels

0;

Gaps

179

Conservative

Search completed: April 15, 2005, 22:51:17 Job time : 339.016 secs

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364 CGCGACANGGCGGCGGCGATC 384

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US-10-156-761-6116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.6%;
Best Local Similarity 47.0%;
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 6116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-08-
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JF 2001-272697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OP INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptomyces avermitilis
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                                                                                                                                                                                                   184 CAGGTGCTCGGCCTCGACCTCGACGAAGCCCTCGCCGCCGCCGCAGGTCTGCGCCCCGGCGTC 243
                                                                                                                                                                                                                                                 850 GCGAAACAGGCCTACTTCGAGTGGGATGCCGGTCCGCCCGGCGATCGAGGGGACCACCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          730 CACAAGGCGGCGGTCGCGATCTGGGACGACCACGAGTTCGCCGACAACGCGTGGTCG
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CCCAMGCTGGACGAGGACATGAAGCGGCGCATCATCGCCCTAATCCTGGAGCGCCGTGAG 363
                                              TOGONGONGGOTOCACGGGONGCGGCNCGGTCGACGACCCGGAGCGTACGCTCACGGGC 102
                                                                                                                                                     GECGECGCGGGAAACCACACCGAGGGCGCCGAGGGCACCTGGACGGCACGTCAGGCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 202;
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Pred. No. 2.3e-05;
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1030 CGGGTCCAGCTCGACTGGCTGAAGGCGCGCGCTCAAGGCGTCCGACACCACCTGGCGGCTG 108

WROWN AMALE TEAS SHIT

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Pred. No. score great and is de Result Ro. Score	Database :	Minimum DB seq Maximum DB seq Post-processin	Title: Perfect score: Sequence: Secoring table: Searched:	OM nucleic - nu Run on:
Addison Microsomo Addison Micro	is the number of results predicted by chanco sacer than or equal to the score of the remarkatived by analysis of the total score distributions of the total score dis	M Commency Libroch4.* 1. gennescyn 150ec.* 1. gennescyn 150ec.*		ticle: US-09-85-3408-6 Perfect moore 14 Segmente: trapppaarcastroopaggtgpcttoggcgrooppga 247 Seoring table: Indrifty NC Seoring table: Indrifty NC Gapon 1070, Caport 1.0 Searched: 430206 sequ; 2959870667 residues Frank number of hits matigifying communications are provided to the provided to th	copyright (e) 1993 - 2005 Compugen Ltd. copyright (e) 1993 - 2005 Compugen Ltd. nucleic search, using sw model April 15, 2005, 14:37:25 Search time 444 Seconds 1993-189 Million cell updates/sec
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### repeat_region 148. 151 ### INVESTED 1892 1892 1892 ### WOODS 1892 1892 1892 ### WOODS 1892 1892 1892 ### INVESTED 1892 1892 1892 ### INVESTED 1892 1892 1892 ### INVESTED 1892 1892 1892 1892 ### INVESTED 1892 1892 1892 1892 #### INVESTED 1892 1892 1892 1892 #### INVESTED 1892 1892 1892 1892 1892 ###################################	OS Micromonospoza estronaeces. ME Novy Location/Salitients PR Novy Location/Salitients PR nike_feature /10.115 Pr nrpeat_region /10.115 Pr repeat_region /10.115 Pr re	8UL 025	14.4 425.7 2 AMM682.0 14.4 425.7 2 AMM123.2 14.4 1200.1 2 AMC782.3 14.4 1200.1 2 AMC782.3 ALIGNMENTS	56 14.6 110000 4 AA15962.39 36 14.6 110000 4 A15962.39 35.8 14.5 678 2 AVV2145- 35.8 14.5 2 AVV2145- 35.8 14.5 3 300 4 AL51266 35.8 14.5 3 300 6 AM21266 35.8 14.5 3 300 6 AM21262 35.8 14.5 30746 8 AM21262 35.8 14.5 30746 8 AM21262	21 36.6 14.8 444 5 AM577999 22 36.6 14.8 734 5 AM577999 23 36.6 14.8 734 5 AM577919 24 36.6 14.8 734 5 AM577910 25 36.6 14.8 1344 6 AM517910 26 36.6 14.8 1344 6 AM513010 26 36.6 14.8 1344 12 AM513010 27 36.6 14.8 7345 7 AM513010 28 36.6 14.8 7345 7 AM513010 29 36.6 14.8 7345 7 AM513010 20 36.6 14.8 745 7 AM513010 20 36.6 1
· 9	*	re DNA. Site; attP; c product; at	Aav68520 The r Aav10362 Infe Aaq76213 HSV	Continuation Continuation Av23145 5' fr Aax84348 Steal Aaz06968 Humar Aac01906 Hg20 Aba93500 Humar Aal61224 Actir Continuation Ah28478 Nucle	Aa877809 DNA e AdG52179 Nove Aa877910 DNA e Aa877910 DNA e Ab211384 Human Adm43902 Nove Adf29195 Huma Adg64032 Nove Aa814651 Nucle Aca4083 Proka Aca4083 Proka Abn97994 PM2

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Matches 247;
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                                     repeat_region
                                                                                         misc_feature
                                                                                                                                                misc_feature
                                                                                                                                                                                                    Micromonospora
                                                                                                                                                                                                                                          secondary
                                                                                                                                                                                                                                                 Integrase; int; excisionase; xis; integrase attachment site; attp; pMLP1 site=geoific integration; hybrid antibiotic; metabolic product; attB;
                                                                                                                                                                                                                                                                                                            Micromonospora carbonacea pMLP1 attB DNA
                                                                                                                                                                                                                                                                                                                                                                                                                    AAD25934 standard; DNA; 241 BP
                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
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Micromotopher carboness was afficiant. Bolymications of the invention 
useful for conting watering the attimospers with a vector. They are also 
continuouses. The integrating waters are useful organization work 
permit, multiplate secondary metabolic pathways and create new metabolic 
products, media. Bylotid antibiotics. The present sequence is public 
products, media. Bylotid antibiotics. The present sequence is public.
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P-PSDB; AAB15909.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resent invention relates to novel polynucleotides encoding integrase and excisionase (xis) and an integrase attachment site (attP) which
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                                                                                                                                                                                                                                      metabolic pathway; ds
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                    carbonacea
                  /*tag=
                                     /*tag= b
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124. .137
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                                                                                                                                                               Location/Qualifiers
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Pred. No. 1e-53;
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           AAXBXI
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Integrase, int; excisionase; xis; integrase attachment site; attp; pMLP1; site-specific integration; hybrid antibiotic; metabolic product;
                                                       Micromonospora carbonacea pMLP1 attP DNA.
                                                                                                26-MAR-2002
                                                                                                                                     AAD25945
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AAD25945 standard; DNA; 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCAL
                                                                                                                                        215
                                                                                                                                                                                                                                                                                                                                                                                     101 GGGTTCAATTCCCATCAGTCACCCGTACACGAAGGCCCCCTCCACTCGGAAGGGGGCCTTC
                                                                                                                                                                                                                                                                                 161 GGCGTTCCTGAGGGTTCGCGGTCAGGCGGTCGGCGCTCGGGGGGACTCGGCCCCGTC
                                                                                                                                                                                                                                                                                                                                     95 GGGTTCAATTCCCATCAGTCACCCGTACACGAAGGCCCCCTCCACTCGGAGGGGGCCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 59.5%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHERING CORP.
                                                                                                                                   GGCGGGAGTGGCCTCGGCGTCCGGGGA
                                                                                                                                                                                  GGCGGGAGTGGCCTCGGCGTCCGGGGA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(179. .241)
/*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "attB peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_type= INVERTED
/note= "Inverted repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_type= INVERTED
/note= "Inverted repeat 1 (IR1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 155
     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 147,
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 0;
                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IR2) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 241
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                 214
                                                                                                                                                                                                                                                                                 220
                                                                                                                                                                                                                                                                                                                                                                                          160
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0

(first entry)

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Matches
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                  are useful for transforming an actinomyces with a vector. They are also useful for creating vectors for site-specific integrated into boat chromosomes. The integrating vectors are used to express actinomycete genes, annipulate secondary searboils pathways and create new metabole products such as it hybrid entiblotics. The present sequence is pMLP1 attP products such as it hybrid entiblotics. The present sequence is pMLP1 attP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hosted TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2000; 2000US-0204670P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-2001; 2001WO-US015760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200187936-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Micromonospora carbonacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  secondary metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (int) and excisionase (xis) and an integrase attachment site (attp) which are isolated from pMLP1, a bacteriphopse (lyeogenic phage) isolated from Micromonopora earbonaces var. africana polymncleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel polynucleotides encoding integrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 4; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transforming an actinomycete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-082983/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                 Sequence 209 BP;
                                                                                                                                                                                                                                                                                                                                                                                                               DNA from Micromonospora carbonaces
                                                                                                                                                                                                                                                                                                Local
                                              121
                                                                                                                                                                                                                                                                        125; Conservative
                                                                                        61
                                                                                                                                  61
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                        GTCAGGTGGCCTGTTGACCCCGTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTC 120
                                                                                                                                  GTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTC
                                                                                                                                                                                                                     TAGGGGAATCCACTCCGGAGACGCCCGGAGCATCCCGGAGCATGACGGAGCAACCAGCAG
Acccd 125
                                              ACCCG 125
                                                                                                                                                                                TACCCCAATCCACTCCCCCAGACCCCCCGGAGCAATCCCGGAGCATCACCAGCAACCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horan AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "attP region"
145. .162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167. .186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101. .125
                                                                                                                                                                                                                                                                                                                                                                     49 A; 64 C; 66 G; 30 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Invertad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_type= INVERTED
note= "Inverted repeat 1 (IR1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                50.6%; Score 125;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Inverted repeat 2 (IR2)"
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                         1.5e-22
                                                                                                                                                                                                                                                                                                                           DB 6,
                                                                                                                                                                                                                                                                                                                           Length 209
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are also
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                                                                                                                                                120
                                                                                                                                                                                              60
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22X8X83
                 11-SEP-2003
26-SEP-2001
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Micromonospora DNA encoding integrase enzymes
                                                                  (first entry)
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Everninomicin; antibiotic; bottle-neck gene; orthomicin; integrase; ds

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misc_feature
                                                                                                                                          Micromonospora
                                                                                                                                          sp. ATCC 39149
                          2570.
                                     /product= "Integrase #2"
                                                                                                                     Location/Qualifiers
                                                                product= "Integrase #1"
394. .2572
                                                                                        *tag=
note= "Att/B/AttP region of
             *tag=
                          .2799
  integrase action
```

CDS

misc_recomb 27114 /label= Insertion_juncture "Site of integrase activity .2715

WO200151639-A2

12-JAN-2001; 2001WO-US001187

12-JAN-2000; 2000US-0175751P

(SCHE) SCHERING CORP.

Hosted TJ, Horan AC, Wang

WPI; 2001-442147/47

P-PSDB; AAU04900, AAU04912

New nucleic acid molecules encoding everninomicin pathway ge-useful for improving yields of everninomicin, to produce new everninomicin and as probes to identify homologous sequences pathway gene pro

Claim 26; Fig 7; 109pp; English

S

une pure membranering monit deventionality. Talked composable, and common and the second and the common and the The asquares excelse 2 integrases which permit site specific integral of a vector into a metiomorpeate, especially a Micromoroppera of a vector into an extramentary and and vectors comprising a M. carbonacea eventimental misory-brief cardia and vectors comprising a M. carbonacea eventimental misory-brief cardia of transference of the vector of medicardor into an additionate eventimental photosphere in a box encoding the hispothesis protein the genum statemental protein and service of the protein and transference of the protein and trans

88888888888

RESULT 4 AAS08694

AAS08694 standard; DNA; 4388 BP

AAS08694;

Streptomyces antibioticus.

field)

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RESULT 5
AAD25939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.6%;
Best Local Similarity 100.0%;
Movel polymucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lymogenic phage pMLP1, useful for transforming an actinomycete.
                                                                           P-PSDB; AAE15910
                                                                                        WPI; 2002-082983/11.
                                                                                                                      Hosted TJ, Horan AC
                                                                                                                                                      (SCHE ) SCHERING CORP
                                                                                                                                                                                    17-MAY-2000; 2000US-0204670P
                                                                                                                                                                                                                     15-MAY-2001, 2001WO-US015760
                                                                                                                                                                                                                                                                                   W0200187936-A2
                                                                                                                                                                                                                                                                                                                                                        Sg
                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Micromonospora halophytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Integraes; int; excisionaes; xis; integraes attachment site; attp; pMLD; site-specific integration; bybrid antiblocic; metabolic product; attB; secondary metabolic pathway; attB/attP DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Micromonospora halophitica pMLP1 attP/attB right juncture DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD25939 standard; DNA; 260 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-2003
26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD25939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4388 BP; 714 A; 1468 C; 1506 G; 694 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2651 GTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCGGTACGGGTTCAATTCCCCATCAGTC 2710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCCG 2715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGGGGANTCCACTCCGGAGACGCCCGGAGCAATCCGGAGCATGACGGAGCAACCAGCAG 2650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAGGGGAATCCACTCCGGAGACGCCCGGAGCAATCCCGGAGCATGACGGAGCAACCAGCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCCG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                           /rpt_type= INVERTED
/note= "Inverted repeat 2 (IR2)"
complement (196, .258)
                                                                                                                                                                                                                                                                                                                                                                                                               155. .166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139. .150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
101. .126
                                                                                                                                                                                                                                                                                                             /product= "attB peptide
                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                               -Eag=
                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Inverted repeat 1 (IR1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "attP/attB region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -Eag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 125;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
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Cao Y, Hinkle GJ,
WPI; 2004-061375/06
New recombinant DNA
for expression of a

recombinant DNA construct comprising a promoter positioned to provide expression of a polynucleotide encoding a polyneptide from a

(CAOY/) (HINK/) (SLAT/)

CAO Y.
HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S
Hinkle GJ,

Slater SC,

Chen X, Goldman BS

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guery Match
Best Local S
21-FEB-2002; 2002US-0360039F
                                                                                                      20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                            18-DEC-2003
                                                                                                                                                                                                                                                                                                        US2003233675-A1
                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogen tolerance, post tolerance, plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield, protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomamam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct; transformed plant; improved plant property, cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADT44391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADT44391 standard; cDNA; 1446 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention cristes to novel polymodection encoding integrate the product of the present invention cristes to novel polymodection encoding integrate the product of the product 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial polynucleotide #19142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 260 BP; 47 A; 83 C; 90 G; 40 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 23; Fig 5; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ACCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide; gene; ss
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100.0%; Pred. No. 2.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 260
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containing an improved property competition that consonting a branch with then the straining an improved property competition that consoltered plant, where the revolutional took controlled is useful for improving plant properties. Co the recombinant public containing plant properties, e.g. improved conditions and the properties of the properties, e.g. improved conditions and thought or pertia. Controlled plants properties, e.g. improved conditions and thought or pertia. Controlled plants properties, e.g. improved conditions to plant disease, better growth rate by modification confidence, improved plant growth regulations, increased rate of content, improved plant growth and development under an least one stress condition, improved light improved rate development in the controlled plants of the province of the content of the province plants of the plants of the
REFERRER
                                                                                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            젖젖
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Best Local Similarity
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transformed plant having an improved property. The plant is a crop plant 
such as make or soybean. The method of producing a transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microbial source. The invention also relates to a trans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1, SEQ ID NO 42829; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a recombinant DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb2 GBAR B receptor, human gb2; Hgb2; calcium-eunsing receptor;
gamma-amino butyric adid, 4-amino butanoia caid, GBAR;
metabotropic glitamate receptor, neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-2 related to human gb2 GABA B receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ29447 standard; DNA; 3396 BP
                                                      02-DEC-1999
                                                                                                                         W09961606-A3
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              psychiatric disorder; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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/note= "The amino aid residue corresponding to basepairs
758 to 760 is not given in the specification"
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(USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                            29-MAY-1998;
J, Bonner TI
                                                                98US-0087274F
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New GABAB (c-aminobutyric acid or 4-aminobutanoic acid) receptor, un for identification of (ant)agonists and for treatment of neurologics WPI; 2000-105616/09 AAY44345.

Disclosure; Page 58; 67pp; English

disorders.

recombinant byte sector comprising byte encoding cobin. The correctionant byte sector comprising byte encoding cobin. The corrections controlled the compression of charge for the sector of pure coopers as most pepthatric disorders, for phreshold physicological, functional, or other investigational analysis of physicological, functional, or other investigational analysis of physicological, functional, or other investigational analysis of physicological, functional, or other controlled the controll The present sequence is a DNA related to human gb 'okba B receptor.
gb2 (HgD2) shares sequence homology with rat caba is receptor gbb,
parathyroid call calcium-ensing receptor and metaborropic glutamatreceptors. It can be produced in host calls by transforming them wi

Sequence 3396 BP; about this sequence in the specification 761 A; 1062 C; 940 G; 633 T; 0 U; 0 Other;

Query Match 15.1 Best Local Similarity 47.1 Matches 115; Conservative 47.34; 0; Mismatches 128; Score 38.2; Pred. No. 3 DB 3; Length 3396; Indels 0

Gap

512 GCGGTGGCGGCGGCGGCGGGCCCGGGCTGCCCCGGAGCTCCGCGGGGAAGCCATGCC 3 GOGGAATCCACTCCGGAGACGCCCGGAGCAATCCGGAGCATGACGGAGCAACCAGCAG

452 GCCGCGGGCTGCGGGCTCACTCGGCCCGCATGGCCTGGCCCGGCCGCCGC 63 CAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCCATCAGT

123 CCGTACACGAAGGCCCCCCCCACTCGGAGGGGGCCTTCGGCGTTCCTGAGGGTTCGCC

392 GEGECANGGTETTECEGEGGGEGECEGEGEANTGGEGCCGGGCCCGGGCTEEG

332 183 CAGGCGGTCGGCTCGGCGCTGGGGGACTCGGCCCGTCGGCGGGGAGTGGCCTCGGCG CGGGCTAGGGTTCCGGCTCGGCTCAGAACGGCCGCGGCGGCGGCGGCGGCGGCGGCGGCG

GGG 245

RESULT 8

AAZ29446/c ID AAZ29 AAZ29446 standard; DNA; 3399

ВP

14-MAR-2000 AAZ29446; (first entry)

DNA-1 related to human gb2 GABA B receptor.

psychiatric disorder; agonist; antagonist; ss metabotropic glutamate receptor; neurological disorder; gb2 GABA B receptor, human gb2; Hgb2; calcium-sensing receptor, gamma-amino butyric acid; 4-amino butanoic acid; GABA;

Homo sapiens

28-MAY-1999;

99WO-US011869

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RESULT 9
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¥888888888
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3399 BP; 760 A; 1052 C; 949 G; 638 T; 0 U; 0 Other:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New GABAB (c-aminobutyric acid or 4-aminobutanoic acid) receptor, useful for identification of (ant)agonists and for treatment of neurological
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                                                          GTG 270
                                                                                                     GGG 245
                                                                                                                              CGGGCTAGGGTTCCGGCTCAGAACGGCCGCGGCGGCGGCGGCGGCAGCGGCGGCG
                                                                                                                                                                    CAGGCGGTCGGCTCGGCGCTGGGGGACTCGGCCCGTCGGCGGGAAGTGGCCTCGGCGTCC
                                                                                                                                                                                                              GCGCCAAGGTCTTÓCCGCGGCGCGCCCGCCAATGGCGCCGGGCCCGGGCCCCGGCTCCGTCT
                                                                                                                                                                                                                                                        CCGTACACGAAGGCCCCCCCCACTCGGAGGGGGCCTTCGGCGTTCCTGAGGGTTCGCGGT
                                                                                                                                                                                                                                                                                                  GCCGCGGGCTGCGGGCGCGGCTCACTCGGCCCGGCATGGCCTGGCCCGGCCGCCGCCGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGAATCCACTCCGGAGACGCCCGGAGCAATCCGGAGCATGACGGAGCAACCAGCAGGT 62
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/note= "the amino acid residue corresponding to basepairs
758 to 760 is not given in the specification"
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Pred. No. 3
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AAZ29422 standard; cDNA; 5786 BP

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09961606-A)
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gamma-maino buryric acid, 4-amino butanoic acci; GABA;
metaborropic glutamate receptor; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psychiatric disorder; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gb2 GABA B receptor encoding cDNA
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183 CMGCGGTCGGCTCGGCGCTCGGCGGGAGAGTGGCCTCGCCGCCCC 242
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                                                                                                                                              GCGCCAAGGTCTTCCCGCGGCGCCCCGGCCAATGGCGCCGGGCCCGGGCCCCGGCTCCGTCT
                                                                                                                                                                                                                              CCGTACACGAAGGCCCCCCCCACTCGGAGGGCCTTCGGCGTTCCTGAGGGTTCGCGGT 182
                                                                                                                                                                                                                                                                                                                       GCCGCGGGCTGGGGCGCCGGGTCACTCGGCCCGGCATGGCCTGGCCCGGCCCGGCCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                       CAGGIGGCCIGITGACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOGGAATCCACTCCGGAGACGCCCGGAGCAATCCCGGAGCATGACGGAGCAACCAGGT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEPT HEALTH & HUMAN SERVICES
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458. .3283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.3%;
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Pred. No. 3
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ABQ14048 ABQ14048 standard; DNA; 662 BP

12-JUL-2002

(first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 639

gastrointestinal; respiratory system; single nucleotide polymorphism; drug; side effect; cancer; central Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; SNP; cell differentiation; ds. nervous system; cardiovascular

Homo sapiens

07-MAR-2002 WO200218632-A2

01-SEP-2001; 2001WO-EP010074

05-SEP-2000; 2000DE-01044543 01-SEP-2000; 2000DE-01043826 (EPIG-) EPIGENOMICS AG

Olek A, Piepenbrock C, Berlin K,

Guetig

diagnosis and prognosis, comprises selective hybridization of from Chemically treated DNA. WPI; 2002-371829/40 of amplicons useful for

Claim 12; 56pp + Sequence Listing; 56pp; German

This invention describes a noval mathod for determining the degree of catchylation of a particular your own of the catchylation of a particular you can be a recent ownered to general small of five, the small is treated observably of the order of particular your catchylation of the order of the catchylation of the particular is an expectate of the small mathod of the order of the particular of the catchylation of the catchy

Query Match Best Local : Sequence 662 BP; 94 A; 93 C; 267 G; 208 T; 0 U; 0 Other;

disclosure of the invention

Local Similarity 15.2%; Score 37.6; Pred. No. 3 Mismatches 3.8; DB 6; Length 662

444 CGGCGGGGGTCGGGTTAGAGGTAGCGGCGCGCGCGATAGTCGGGGCGTTAGCGG

RESULT 11 ABQ14049/c

B S

207 GACTCGGCCCGGTCGGCGGGGGAGTGGCCTCCGGGGGC246

ABQ14049 standard; DNA; 662

ABQ14049

12-JUL-2002 (first entry

Oligonucleotide for detecting cytosine methylation SEQ ID Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis NO 640

ξ gastrointestinal; respiratory system; single nucleotide polymorphi SNP; cell differentiation; ds. drug; side effect; cancer; central nervous system; |cardiovascular

Homo sapiens.

ΧB 07-MAR-2002 WO200218632-A2

PR 01-SEP-2000; 2000DE-01043826 05-SEP-2000; 2000DE-01044543 01-SEP-2001; 2001WO-EP010074

Olek A, (EPIG-) EPIGENOMICS AG Piepenbrock C, Berlin K,

WPI; 2002-371829/40

Determining the degree of cytosine methylation in genomic DNA, usef diagnosis and prognosis, comprises selective hybridization of ampli diagnosis and prognosis, con from chemically treated DNA

Claim 12; 56pp + Sequence Listing; 56pp; German This invention describes a novel method for determining the degree

LILE, INTERNACIO GENERALES E MERCE SERVICIO DE SERVE SICURGE. DE CONTRET.

CONTROLLE SERVE SERVE

Sequence 662 BP; 208 A; 267 C; 93 G; 94 T; 0 0 0

Query Match Best Local Similarity Matches 61; Conserv 15.2%; Score 37.6; D Pred. No. 3.8; 0; Mismatches DB 6; Length 662; otner;

Conservative 61.0%;

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ACC50956/c
ID ACC509
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                                                                                                                                 Matches 113;
                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               caccide the human bladder concern services growers grow in small to the Assay and the Common of the 
                                                                                                                                                                                                                                Sequence 5786 BP; 1414 A; 1672 C; 1474 G; 1226 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for detecting a bladder concer-
associated transcript in a coll from a patient. The method comprises
contacting a biological sample from the patient with a polymicactide
that edictively byperdides to a equanos that is 80 a polymicactide
that delectively byperdides to a equanos that is 80 a polymicactide
table of sequences (see ACC50931 to ACC5169) ACC50931 to ACC5169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 230-231; 307pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patient, comprises contacting a biological sample from the patient with biadder cancer-associated polynucleotide or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a bladder cancer-associated transcript in a cell from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-201532/19
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13-NOV-2001; 2001US-0350666P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss
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515 GCGGTGGCGGCGGCGGGCCCCGGGGCTGCCCCGGAGCTCCGCGGGCAAGCCATGCCGC 456
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                                                     еверальтеслегосовивансоссованосителеваносителеваносиносивельного 62
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                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0302814P
2001US-0310099P
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                                                                                                                                                   15.1%;
                                                                                                                      Score 37.4; DB 8;
Pred. No. 5.3;
0; Mismatches 126;
                                                                                                                                                                                 Length 5786,
                                                                                                                      Indels
                                                                                                                      0;
                                                                                                                Gaps
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pancreas, prostate, skin and uterus),

wounds, ischaemia, heart diseases

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ACC72791/c
ID ACC72
related door includate measures which scrows the process given in Ambiest to Amesing, Also described till describing the presence of amesing of a pathological cell in a patient (2) an expression vector computing the presence (1) an include an expression vector computing the vector (4) an include process (1) and the polyage the mutoke acid, (3) an anthody that predicted by bind the polyage the cell (1) appetited by the process of the proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or done regulated in specific cancers (e.g. about 1011 genes up-regulated for accurate the properties of the genes that are up-regulated for accurate lymphocytic laukemia). ACC/2661 to ACC/2860 represent cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 694-696; 767pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kew genes that are up-regulated or down-regulated in cancers, useful as markers for disposing e.g. cancer, inchesia or heart disseases, or as therepautic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-354600/33
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08-FEB-2002; 2002US-0355257P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer; diagnosis; screening, modulator; leukaemia,
heart disease; atherosclerosis; endometriosis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-2003
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Matches Query Match

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63 ω pathologies drug screening, atheroscierosis

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The invention relates to a movel polymuthestick encoding a gamestine triphosphase binding protein complet receptor (GEV). A polymuthestick entrolled to properties on the protein triphosphase binding protein complete receptor (GEV). The polymuthestick end polympitch as manusant governing the protein triphosphase binding protein completed receptor. The line polymuthestick ender GEVP of the polymuthestick and the great of the polymuthestick and the great of the polymuthestick enders great of the
                                                                                                                                                          Claim 1; SEQ ID NO 1463; 28pp; English
                                                                                                                                                                                          New polymicleotide, useful for preparing a composition for treating a 
patient in meed of increased or suppressed activity or expression of t 
guanosine triphosphate-binding protein coupled receptor.
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for treating these
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                                                                                               Goff SA,
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26-SEP-2001; 2001US-0325448P
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A, Katagiri F,
                                                                                                                                                                                          PROVART N.
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KATAGIRI F.
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                                                                                                                                                                      RICKE D.
                                                                                                                                                                                                                                                                      GLAZEBROOK J
                                                                                                                                                                                                                                                                                              COOPER B
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                                                                                       Moughamer T, Brig
staciri F, Kreps J,
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                                                                                                               Briggs SP,
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RESULT 14 ADC87010/c

183 395 123 455

> Sequence 349999 BP; 91105 A; 78863 C; 81174 G; 98857 T; 0 U; 0 Other DB 10,

GGGGAATCCACTCCGGAGACGCCCCGGAGCAATCCGGAGCATGACGGAGCAACCAGCAG 126; Indels Length 349999; 0; Gaps

255 GCGGTGGCGGCGGCGGGCCCGGGCTGCCCGGAGCTCCGGGGGAAGCCATGCCC

COSTACACGAAGGCCCCTCCACTCGGAGGGGGCCTTCGGCGTTCCTGAGGGTTCGCG

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augmentation; cereal;

soybean, alfalfa, sunflower, canola, cotton, peanut; tobacco; sugar maize; barlay, sorghum, rice; wheat, crop plant; injecticide resists stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apidal dominance; dwartism; early flowering; antivi

Provart N, Ric Ricke Glazebrook J ģ

¥88888888 XX

> Suwa M, (ADSC-)

XAT Asai K,

EP1270724-A2 Homo sapiens Human GPCR gene 01-JAN-2004 ADC87010

gene,

New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of or proceins, resistance to insacticides, virus or fundi, stress tole or high matricional value.

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A Calain 25, 880 ID NO 1271; 200pp; Highish.

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Scoring table:	Title: US-0 Perfect score: 247 Sequence: 1 to	Run on:
IDENTITY_NUC Gapop 10:0 , Gapext 1.0	US-09-855-340B-6 247 1 teggggaatccactccggaggtggcctcggcgtccgggga 247	April 15, 2005, 14:40:40 (statout alignosts) (statout alignosts) 6223.837 Million cell updates/sec

Total number of hits satisfying chosen parameters: Searched: 4708233 seqs, 24227607955 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl: * gb ba: gb_sts:* or a om:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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-	247	100.0	247	6	AX338975	
٠,	147	,,,	241	5	AX338973	AX338973 Sequence
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יה	90	36.4	145	_	AY150028	AY150028 Micromono
10	70	300	143	-	AY150032	AY150032 Micromono
	2	7	33064	N	AY338477	AY338477 Streptomy
		17	175217		AC079680	AC079680 Mus muscu
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c 12	41.4	16.8	36654	ø	AF315943	
c 13	41.4	16.8	55590	9	AC073128	TO TO
0 14	41.4	16.8	152129	2	AC027416	
15	41.4	16.8	310550	ш	SC0939113	ALMOSTIC SCIEDURY
16	41.2	16.7	5966	_	SAMY18862	TERREZ SCERPCOMYCE
0 17	41	16.6	301443	۳	AE017239	AEUL/239 Mycobacca
18	40.8	16.5	16.5 600	,	MLTRNAGC	AUGUST PL. Lucius B
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	37.4	37.6	37.6	37.6	37.8	38	38	38.2	38.2	38.4	38.4	38.4	38.6	38.8	39	39	39.2	39.2	39.2	39.4	39.8	39.8	39.8	39.8	40	40.2	;
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	MALISO7. Sequence 6 from Patent WOO187936. Sequence 6 from Patent WOO187936. MAJ38975.1 Gf:18129111 Micromonospora carbonacea
MSIN	Micromonospora carbonacea Bacteria, Actinobacteria; Actinobacteridae; Actinomycetäle Micromonosporineae; Micromonosporaceae; Micromonospora.
RENCE	

REFER SOURC KEYWO VERSI 1.OCUS

JOURNAL TITLE AUTHORS ACCESSION RESULT 1 AX338975

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linear

PAT 09-0

I melation of MicrosonSpore carbonaces var africans publi in and use of integrating function for site-specific integration MicrosonSpore halpenticas and MicrosonOsSpore carbonaces ch Patent: NO 0187956-A 6 22-NOY-2001; S Hosted, T.J. and Horan, A.C.

FEATURES source /organism="Micromonospora carbonadea" /mol_type="unassigned DNA" /db_xref="taxon:47853" Location/Qualifiers

ORIGIN Matches 247; Query Match Best Local Similarity 1 TAGGGGAATCCACTCCGGAGAGCCAGGGAGCAATCCGGAGCATGACGGAGCAACCAG TAGGGGAATCCACTCCGGAGACGCCCGGAGCAATCCGGAGCATGACGGAGCAACCAG Conservative 100.0%; Score 247; DB 6; 100.0%; Pred. No. 2.4e-37; tive 0; Mismatches 0; Length 247; indels

0 Ga

61 GTCAGGTGGCCTGTTGACCCCCTGACCAGGCCCCGGTACGGGTTCAATTCCCATCA 61 GTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATGA

181 GTCAGGCGGTCGGCTCGGCGCTCGGGGGACTCGGCCGGTCGGCGGGAGTGGCCTCGC

source

	Discourt view Mexic(,D.D. and Alexander,D.C. Discourt Shahiston Mexicourty and Alexander,D.C. Submitted (12-85P-2002) New Lead Discovery, Schering-Plough	JOURNAL
Source	In Micromonopoza gp Micromonopoza gp Microbiology (Reading, Engl.) 149 (Pt 9), 2443-2453 (2003) 1289170. 2 (Dames 1 to 145)	JOURNAL PUBMED BFERENCE
JOURNAL	romonospora carbonacea var. afri LP1 integrase for site-specific	TITLE
JOURNAL PUBMED REFERENCE AUTHORS TITLE	Miccomonspora mp. ATCC 39149 Miccomonspora mp. ATCC 39149 Miccomonspora mp. ATCC 39149 Miccomonsportamp. ATCC 39149 Miccomonsportamp. Miccomonsporamene, Miccomonspor	ORGANISM ORGANISM DEFERENCE AUTHORS
REFERENCE AUTHORS TITLE		ACCESSION FERSION ERSION EYWORDS
VERSION KEYWORDS SOURCE ORGANISM	V150033	RESULT 3
AY150027 LOCUS DEFINITION ACCESSION	SUSTITICTIONAGGITTOGOGITCAGGGGTCGGGCGTTGGGGGATCGGGGATCGGCGTTGGGGGATCGGCGTCGGGGATCGGGGGATCGGGGGGATCGGGGGGATCGGGGGGGG	8 8 8
B		. 8
Q	,,	등 &
DB QV	Query March 19.59, Score 147; DB 6; Length 241; Best Local 161mlarity 100.00; Pred. No. 2.8e-18; Matches .147; Conservative 0; Missacches 0; Indels 0; Gaps 0;	Query Ma Best Loc Matches
F 5	/do_xrer="taxon:47853"	ORIGIN
Query Ma Best Loc Matches		FEATURES
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Bourg	× 9	RESULT 2 AX338973 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS
		ъ
FEATURES	181 OTCHGECTOGCCCCTGGGGCTTGGGGGCCCCGTCGGCGGAGTGGCCTCGGCGT 240 241 CCGGGGA 247	S B

. R

/note="host is deposited in ATCC as Micromonospora carbonacea var. africana Waitz et al."

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wory Match 58.7%; Score 145; DB 1; Length 145; Bet Local Similarity 100.0%; Pred. No. 7.7e-18; Indels atches 145; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 TCCTGAGGGTTCGCGGTCAGGCGGT 190
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                                                                                                                                                                                                                                  Submitted (12-SEP-2002) New Lead Discovery, Schering-Plough Research, 2015 Galloping Hill Road, Kenilworth, NJ 07033, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CANTTCCCATCACTCACCCGTACACGAAGGCCCCCCCCACTCGGAGGGGGGGCCTTCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Hosted, T.J. Jr., Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development of the Micromonospora carbonacea var. africana ATCC 33149 bacteriophage MMEP integrate for site-specific integration in Micromonospora spp Micromonospora
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2025 bp
Bacteriophage pMLP1 att/int region.
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Alexander, D.C., Devlin, D.J., Hewitt, D.D., Horan, A.C. and
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Bacteriophage pMLP1
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1. .145
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Location/Qualifiers
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	OV 106 CAMPTOCCAPCHOCTOLCC 124 Db 61 CAMPTOCCAPCHOCTOLCC 79
	Oy 46 CGBACCHACCACCACCACCACCACCACCACCACCACCACCACC
	Query Match 22.0%; Score 79; DB 1; Length 143; Best Local Smilarity 100.0%; Park. No. 2.9e.65; Matches 79; Conservative 0; Missachies 0; Indols 0; Gaps 0;
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* * *	
COMMENT on Co	
	PUBMED 1949170 (Needing, Engl.) 149 (Pt 9), 2443-2453 (2003) REFERENCE 2 (bases 1 to 143)
TITLE Dir	JeveLopment of the Micromonospora 39149 bacteriophage pMLP1 integras in Micromonospora app
REFERENCE 3	
IPR Tec	Bacteria: Actinobacteria: Actinobacteridae; Actinomycetales; REFERENCE Micromonoportanee; Micromonospora. 1 (bases 1 to 143)
	SOURCE Migromonospora nigra ORGANISM Migromonospora nigra
JOURNAL Ant PUBMED 147 REFERENCE 2	region.
TITLE Fun	AY150032 1
AUTHORS Pan	RESULT 7
Str	Db 116 GGCGTTCCTGAGGGTTCGCGGTCAGGCGGT 145

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ALQILRNVRAAIKPGGRLLIAEMVIPEQGDEPHSGKLVDLWLMLLVGGRERTPGQYAD LLARAGERLERVVETAAAISLVEAVPV" CORRENTINIENT NOTICE DE LE CONTROL DE LA CON

(reans1 table=1)
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/evidence=not_experimental

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to Pfam PF00891 O-methyltransferase*

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by the segmonce will be replaced by the finished segmence as soon as it is available and the accession number will be preserved in the second of the second 
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Oct 7, 2004 this sequence version replaced gi:39748104
NOTE: This is a "working draft' sequence. It currently
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TR 110, Universite Henri Poincare, Faculte des Sciences et
chniques, Boulevard des Ajguillettes, BP 239,
ndoeuvre-les-Mancy 54 506, France
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TR 110, Universite Henri Pointonero, Faculte des Sciences et
chiniques, Boulevard des Aiguillettes, BP 239,
Indoewrre-les-Hancy 54 506, France
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     Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
(bases 1 to 194452)
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 10, clone RP23-60H16 (Dases 1 to 194452)

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Submitted (09-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge MA 0211, USA On Mar 2, 2004 this sequence version replaced 91:24182664. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html -- Genome Center

Contact: sequence_submissions@genome.wi.mit.edu Web site: http://www-seq.wi.mit.edu Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR

Center clone name: Center project name: L23285 91 H 16

Sequencing vector: Plasmid; n/a; 100% of reads

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No. 1.3ee02; Indels 0; Casarathee 67; Conservative 0; Mismatches 41; Indels 0; Casarathee 67; Casarathee 67</td> <td></td> <td>REPEKKRONTFUNDILSGESERSVOLARILAMASSYNLVALDETTULDALALA TREPTLYVENSHDEXILERVCDTSTRCSATGS" 1932. ; 1963 terminator 1932. ; 1963</td> <td>ARTINIA MARIATI SANTI SA</td> <td>TLLEVLSGGYDRGRYGRGRRRRRGRYTTKYTTVLGYTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT</td> <td>db xref="Unibrot/TrEMBL:054072" /tramslation="WVNLINLESVEKEYGVRFLLDEVSLAVGASDRIGVVK/tramslation="WVNLINLESVEKEYGVRFLLDEVSLAVGASDRIGVVK/tramslation="WVNLINLESVEKEYGVRFLLDEVSLAVGASDRIGVVK/tramslation="WVNLINLESVEKEYGVRFLLDEVSLAVGASDRIGVVK/tramslation="WVNLINLESVEKEYGVRFLLDEVSLAVGASDRIGVVK/tramslation="WVNLINLESVEKEYGVRFLLDEVSLAVGASDRIGVVK/tramslation="WVNLINLESVEKEYGVRFLLDEVSLAVGASDRIGVVK/tramslation="WVNLINLESVEKEYGVRFLLDEVSLAVGASDRIGVVK/tramslation="WVNLINLESVEKEYGVRFLLDEVSLAVGASDRIGVVK/tramslation="WVNLINLESVEKEYGVK/tramslation="WVNLINLESVekeygvk/tramslation="WVNLINLESVekeygvk/tramslation="WVNLINLESvekeygvk/tramslation="WVNLINLESvekeygvk/tramslation="WVNLINLESvekeygvk/tramslation="WVNLINLESvekeygvk/tramslation="WVNLINLESvekeygvk/tramslation="WVNLINLESvekeygvk/tramslation="WVNLINLEsvekeygvk/tramslation="WVNLINLEsvekeygvk/tramslation="WVNLINLEsvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNLinlesvekeygvk/tramslation="WVNlinlesvekeygvk/tramslation="WVNlinlesvekeygvk/tramslation="WVNlinlesvekeygvk/tram</td> <td>/protein_id="0A556726.1" /db_xref="0G1:530357"</td> <td>/trans table=11 /trans table=11 /product="putative ABC tranporter"</td> <td>/standard name="EFEX" /oitation=[1]</td> <td>CDS 3751820 /gene="ertX"</td> <td>gene 3751820</td> <td>RBS 358363 /citation=[1]</td> <td>-10_signal 317323 /citation=[1]</td> <td> /strain="NCIMB 8594" /db xref="taxon1836"</td> <td> FEATURES Location/Qualifiers</td> <td>TITUE DIRECT CHARACTER 1994) M. O'Neill, Department of Microbiolo JCURNAL Submitted (29-UUL-1994) M. O'Neill, Department of Microbiolo JCURNAL Submitted (199-UUL-1994) M. O'Neill, Department of Microbiolo JCURNAL Submitted (199-UUL-199-</td> <td>R CE</td> <td></td> <td>ž</td> <td>REPERENCE 1 LAURE FOR TO INC. Bayers. A., Radford, A., Baumberg, S. and Cove, J.I. AUTHORS O'Neill, M.F., Eady, S.A., Radford, A., Baumberg, S. and Cove, J.I. The use of PCR to isolate a putative ABC transporter from</td> <td>Pac</td> <td>KEYNUKUS ABU UKAMPULUEN. SOURCE Sacchharopolyspora erythraea ORGANISM Sacchharopolyspora erythraea</td> <td>-</td> <td>~</td>	Oy 138 CCTTCDAFCGBAGGGGGCTCCGCTCGGGGTTCGGGGTTCGGGGTTCGGGGTTCGGGGTTCGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG	Overy Match 17.2%; Score 42.4; DB 1; Longth 1976; Best Local Similarity 6.0%; Pred. 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Submitted (04-UU-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, UBA
                                                                                                                                  Direct Submission
                                                                                                                                                                                 5 (bases 1 to 55590)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (14-MAY-2002) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) (bases 1 to 55590) ...www.ws; Catarrhin. Sulston, J.E. and Waterston, Recovered complete human genome sequence denome Res. 8 (11), 1097-1108 (1999) 9962792
                                                                                                                                                                                                                                                                     MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.H.
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of Homo sapiens BAC clone RP11-64705 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 ACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCCATCAGTCACCCGTACACGAAGGC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris, A. and Kozlowicz, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9847074
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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HOmo sapiens BAC clone RP11-64705 from 2, complete sequence.
AC07318
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                                                                                                                                                                                                                                                                                        Sequencing Center, Washington
4444 Forest Park Parkway, St. Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping

Web site: http://genome.wustl.edu/gsc

Waterston, R.

(bases 1 to 55590)

Direct Submission

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping information for this clone was provided by Dr. John D. 
WcPherson, Department of Genetics, Washington University, St. Louis 
WO. For additional information about the map position of this 
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        all regions were double extraded, sequenced with an alternate classifier constitution of the constitution 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone sections once, or longer because we provide a small overlap
between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Data from AC092152 was used to finish this clone, AC092152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the left is RP11-459119, 2000 by overlap; the clone sequenced to the right is RP11-3104, 2000 bp overlap; the clone sequenced to the right is RP11-3104, 2000 bp overlap; actual start of this clone is at base position 13291 of RP11-3304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAPPING INFORMATION
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and coworkers at http://www.chori.org
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8932. .9040
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7951. 8074
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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'rpt_family="MIR"
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3493. .14286
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36132. .36381
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5. .26248
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1. .34624
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AC027416/c
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Best Local :
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88 Streen, B. Littori, J. Nabaum, C., Lander, F., Abraham, H., Allen, N., Bestlen, Y., Bedd, F., Abraham, C., Canton, J., Bedd, F., Abraham, C., Canton, C., Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19886 GGAGCAGGGAGCCAGCGGTGGGGGGGTGGGTGGGG 19852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20006 AGCTCCTGTTCAGGGCCCCAGTTTCGGTTCTGGCCCCAGCTGTCTGGGGCAGACACACGC
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                                                                                                                                                                                                                                                                                                                                                                                                            On Jun 7, 2000 this sequence version replaced gi:7342115 All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 ACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTCACCCGTACACGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-504G11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia, Eutheria, Pr
1 (bases 1 to 152129)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BukaryOta, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unordered pieces
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Center project name: L7458
Center clone name: 504 G 11
------ Summary Statistics
Sequencing vector: M13; M77815;
                                                                                                                                      Contact: sequence submissions@genome
Project Information
                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                 Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                       A.F.A. & Green, P. (1996-1997)
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Pred. No. 7
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MENCE, 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will
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Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in 220 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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Assembly program: Phrap; version o.
Consensus quality: 13376 bases at
Consensus quality: 143264 bases at
Consensus quality: 145203 bases at
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LPATVERSTESTHJADRESMOGRILSREHRYCLSVIHHINDRYTAVAAELALMAGADRI
BGCLEGGBETGAVILVILVAMILSREHRYCLSVIHHINDRYTAVAAELALMAGADRI
GGGBETGAVILVILVAMILSREHVCLSVIHHINDRYTAVAAELALMAGADRI
VODLYTTSESGSHODALKKGFDAMEDDAARGVTVDDIEMAVPYLPIDPKDVORSYBA
VODLYTTSESGSHODALKKGFDAMEDDAARGVTVDDIEMAVPYLPIDPKDVORSYBA
/gene="SCO2528"
                                                               /note="Pfam match to entry PF00682 HMGL-like, , score 204.40, E-value 1.8e-57"
                                                                                                                                                                   complement (2244. .3029)
/gene="SCO2528"
                                                                                                                                                                                                                                                                                                                              VIRVNSQSGKOGIAYVLKNDHSLDLPRRMQIEFSKLIQAKTDABOGEITFTAIWDVFQ
DBYLFNIDNFWGRIQVAKGQTTTDRDGVDTLTVDATVDGAETTLVGSGNGFISAFFHA
                                                                                                                                                                                                                                                                                         LQGVGIDVRLLDYQEHTMSEGASAQAASYIBCAIGDKVLWGIGIDANTTRASLKAVVS
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misc_feature misc_teature /note=*99 % identical to Streptomyces coelicolor TR:031046 EMBL:AF026444) leuk leader peptide and /note="PS00816 Alpha-isopropylmalate and homocitrate synthases signature 2" complement(2912. .3574)

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2-isopropylmalate synthase (leuh) gens, complete cds." complement (3072. .1122) /gens="SCO2528" synthases signature 1* note="PS00815 Alpha-isopropylmalate and homocitrate mplement (3263.

CDS gene misc_reatur

gene="8C02529"

/note="synonym: SCC117.02"

scores opt: 659 z-score: 721.0 E(): 9e-33 41.2% identity Highly similar to several including: Serratia marcescens SH:SMP SERM. (EMBL: M9585) extracilular minor minor metalloproteass precursor (EC 3.4.24.) (352 aa), fasta note="SCC117.02, gene="SC02529" possible metalloprotease, len: 356 aa

in 391 as overlap and Envinis carciovora subsp. carcococca 88:2872. EMRON (EMRU-M96551) extraolillate medilupratesse precursor (EC 34.434-) (347 as), fasta accose opt: 1151 2-800es 1354, 081; 10: 49 64 identity in 349 as overlap. Concasna a Fiem mucch to entry PP11447 Peptidaes M. Dermolyjein femily, Peptidaes and a Frestei kit to 60014. signature. Neutral zinc metallopeptidases, zinc-binding region

/codon_start=1 /transl_table=11

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misc_teature gene="SC02529" 3746. .4669

misc_feature /notes-Pfam match to entry PF01447 Paptidase_M4, Thermolysin family poptidase, score 252.10, E-value 7.7e-72" /note="PS00142 Neutral zinc metallopeptidases, zinc-binding region signature." "gene="SC02529"

gene="SC02530" note="SCC117.03, unknown, len: 88 aa." 706. .4972 gene="SC02530" SCC117.03

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SCC117

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Best Local Similarity 12.0%; Pred. No. 0.043;	ORIGIN 19.9%; Score 49.2; DB 9; Length 925;	(mo.) Lype="geomic MAN" (do.) Set#s second 292" (close) Jbb="86016-99" (close) Jbb="86016-99" (close) Jbb="86016-99" (close="geomic 1873")	found at http://batpac.med.buttalo.edu/dromphila_we FEATURES Location/Qualifiers Bource 1925 Jorganiam="Dromophila melanogaster"	pi and EST libraries. A more detailed description of the 11 pi and EST libraries and law to order individual BAC clones, the entire library. A side the content of the BACPAC Resource RES	NY. The library is named RPCI-98 and was constructed by par NY. The library is named RPCI-98 and was constructed by par EcoRI digestion of Drosophila DNA provided by the BOOF from incomple arrain y2; on bw sp. the same strain used for the	Passes are littp://www.fristfly.org The BDGD prosophila and a passes are littp://www.fristfly.org The BDGD prosophila and a passes are litterary was prepared by Kabautoyo Gunospare and Litterary was prepared by Kabautoyo Gunospare and Literary and Literary (a Literary and Liter	COMMENT Collaboration with the Berkelay Drosophila (Genome Project (E Collaboration with the Berkelay Drosophila (Drosophila Constructing a physical map of the Drosophila The Bogs is constructing a physical map of the Drosophila Collaboration of the Dros	i	REFERENCE 1 (Dames à 100 9-2) AUTHORS Genoscope . TITLE Direct Submission . TOTAL Direct Submission . TOTAL DIRECT SUBMISSION . TOTAL	Dro Buk Eph	RESULT 1 CMS0001F/C MS0091F1 DEFENTION DECEMBER 2525 Dp DNA 11near GSS 03-U LOCUS DEFENTIONS DECEMBER melanogament genome durvey sequence TET3 end of B	ALIGNMENTS		4 15.5 646 6 CD422225	38.4 15.5 522 7 CP569480 38.4 15.5 602 6 CB875859	38.4 15.5 376 5 8U996209 38.4 15.5 405 5 8U999117 38.4 15.5 434 5 8U997816 38.4 15.5 434 6 CB859042	33 38.6 15.6 581 6 34 38.6 15.6 696 9 35 38.6 15.6 1115 36 38.4 15.5 305 1	39 15.8 1367 7 CV068980 38.8 15.7 870 9 CC626829 38.6 15.7 447 2 BF145773	9 CNSO052P 8 B09283 7 CNO16299	16.0 1051 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation of 10,154 expressed sequence tags from a leafy gametophyte of marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
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Kazusa DNA Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyra yezoensis
Bukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
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PM015b0g r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Erika Asamizu
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                                                              CGCAGTGCGAĞCGĞCTGGĞAĞCĞATĞAAĞGCCĞCCĞĞĞĞACGACĞĞĞĞGGĞTĞGĞĞĞĞĞ 272
                                                                                            CCACTCGGAGGGGCCTTCGGCGTTCCTGAGGGTTCGCGGTCAGGCGGTCGGCTCGGCGC 201
                                                                                                                             CTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTCACCGTACACGAAGGCCCCCT 141
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                                                                                                                                                                                                                                                                                      /clone_lib="Borphyra yezoensis TU-1"
//note="Vector: pBluescriptII SK.; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                  /organism="Porphyra yezoensis"
|mol_type="mRNA"
|strain="TU-1"
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VERSION

5', mRNA sequence. BM554300 BM554300.1 GI:18793782

1229 AGENCOURT 6581004 NIH MGC_41

Homo

mRNA linear EST 20-FEB-2002 sapiens cDNA clone IMAGE:5469357

BM554300

799 \$3659CG\$\$8\$65\$CGGG\$6CC\$\$GC\$\$GC\$\$GCGCCC\$\$GCGCGCG\$.853

CGGCTCGGCGCTGGGCACTCGGCCCCGTCGGCGAGTGGCCTCGGCGTCCGGG 245

133 AGGCCCCCCCACTCGGAGGGGCCTTCGGGGTTCCTGAGGGTTCGCGGTC--AGGCGGT 190

191

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GITGACÇÇCCTGAÇCAĞGGCCÇCGGTAÇĞGGTTCAATTCCCATCAGTCACCCGTACACGA 132

83,

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h 18.5%; Score 45.8; DB 9;
Similarity 35.3%; Pred. No. 0.31;
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Dukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosephilidae; Drosephila
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                      /note="end : T7"
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Drosophila melanogaster
Drosophila melanogaster
Skaryota, Metazasi, Arthropoda, Hasapoda, Insecta, Pterygota,
Noppiers, Endopergota, Dipters, Branchovers, Mascomorpha,
Bohydroides, Drosophildae, Drosophila
                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="lymphoblast"
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Department of Biological Sciences California State University San Marcos 333 S. Twin Oaks Valley Road, San Marc

San Marcos, CA 92096-0001, USA

Unpublished (2003

Contact: Betsy Read

Marine Coccolithophorid, Emiliania huxleyi

Analysis of Expressed Sequence Tags from Calcifying Cells of the Wahlund, T.M., Hadaegh, A.R., Clark, R., Nguyen, B., Fanelli, M. and

Bukaryota, Haptophycese; Isochrysidales; Emiliania (bases 1 to 934)

Emiliania huxleyi Emiliania huxleyi CF753549.1 GI:37697342

Email: bread@csusm.eq

/mol_type="mRNA" /strain="1516" /organism="Emiliania huxleyi" Location/Qualifiers 760 750 4129

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Source
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                                                                                                                                                                                    846 SVCGSSRSSSGSGVGVSRVRSSMCSCSCGSSMCSSRSGGCGCSCGGSSCCSSSGSASGSG
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                                                                                                                                                                                                                                                                                                                788 CCSCSCSSCCMVVASSVKSCCCMACMGSCCCGCGSCASGSMCCGCCCCCC--SVASAAGR 845
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CF-03-04 by MRNA linear EGT 16-OCT-20 EST-COntig388 Preamplified custom cDNA 11brary in pMASS8 (ResGen, Invitrogen Inc.) Emiliania huxleyi cDNA, mRNA sequence.
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/db_xref="taxon:7227"
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Pred. No. 2.5;
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/note="Organ: leaf, Vector: pBCSK(;); Site_l: HinoI prepared from purified nuclei was randomly sheared,	Tel 81-5-503-911). Fax:81-45-503-9170) COMMENT Clones are derived from the chimpanzee BAC library FTB This BAC end
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BOUTCE 1726 /organiem "Sorghum bicolor" /mol_type="genomic DNA"	8 6
	AUTHORS Polykyma.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., TOKA: NOTICE TO A TOYON TO THE TOYON TOYON TO THE TOYON TOYON TOYON TO THE TOYON TO THE TOYON TOYON TOYON TO THE TOYON THE TOWN THE TOYON THE TOWN THE THE TO
401 Eccept Bark Ave, St. Louis, wo salve, con galve, loss Sys Pax: 314 613 5979 Pax: 314 613 5979 Email: jbdefileoricongenomics-com Email: jbdefileoricongenomics-com	SOURCE Pan troplodyces (cnampusser) SOURCE Pan troplodyces (cnampusser) OROMNISM Pan troplodyces Dakaryous Metzoa; Opcdes; Consists, Vertebrats; Butaleostomi; Dakaryous Momania; Butbesta; Primates; Octarthini; Hominidae; Pan.
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Robbins, D., Rohling, T., Stantour, N., Lakey, N. and Bedell, J.A. Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A. Trille Genefhresher methylation filtered genomic sequences from Sort bicolor	RESULT'9 AG136795/c AG136795 DEERNITION Pan troglodytes DNA, clone: PTB-150818.F, genomic survey sequence.
REFERENCE 1 (bases 1 to 726) AUTHORS Budiman, M.A. Filck, B., Jones, J., Numberg, A., Citek, R.W.,	
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GSS. Sorghum bic	660
sequence. ACCESSION CL147646.1 GI:40647662	OY 148 GENGGEGCTTCGGCGTTCCTGNGGGGTCNGGCGGTCNGGCGTCGGCTCCGGCGCTCGGCGC

MeBLICE, A., Framer, C.M., Buddman, M.A., Bedell, J. TITLE CIRCLE R.W. Numberg, A., Robbins, D. and Lakey, M. JOURNAL TRANSLAND (2012) COMMENT CONTROL CARP (ARREST OF COMMENT CONTROL CARP) CONTROL CARP (ARREST OF CONTROL CARP) CONTROL CARP (ARREST OF CONTROL CARP) CONTROL CARP (ARREST OF CARP) CONTROL CAR	Spermatophyte, is Magnolophyte, it.liopsida; clade; Pantcoideae; Andropogoneae; Zea. REFERENCE 1 (bases 1 to 839) AUTHORS . Whitelaw, C.A., Quackenbush, J., Van Aken, S.	N.	seque 31996	×	RESULT 12	9y 211 0000000000000000000000000000000000	97 151 GGGGCTTCGGGGTTCCTGAGGGTTCAGCGTCAGCCGTCGGGGAGCAGCTGGGGGACTTCGGGGTTCCTGAGGGTTCCTGGGGGTCGGGGAGCAGCCGGTCGAGCGTCGGGGTCGAGCGGTCGAGCGTCGAGCGTCGAGCGTCGAGCGTCGAGCGTCGAGCGTCGAGCGGTCGAGCGGTCGAGCGAG	308	91	Oy 31 CAATOCGGAGCATGACGGAGCAACCAGGAGGTCAGGTGGGCCTGTTGACCCCCCTGACCAGG	Hest Local Similarity 49.5%; Pred. No. 4.4; Matches 106; Conservative 0; Mismatches	y Match 16.7%;	/note="vector: pBCSK., Site methylation filtered genomic	/db_xref="taxon:4577" /clone="ZMMBMa0585G07" /clone_lib="ZM_0.7_1.5	/organismm="cea mays" /mol_type="genomic DNA" /strain="873"	ualii		9712 Medical Center Drive, Rockville, Tel: 301-838-5843 Fax: 301-838-7008	AL Unpublished (2 Other GSSs: OG Contact: Cathy	nbush,J., M., Budima ., Robbins	Spermatophy clade, Pan l (bases
	Poales; Poales	,		DNA linear GSS 19-JUN-2003 Genomic Clone ZMMRMAD1844F04	*	06 244 	CAGGCGGTCGGCTCGGGGGGACT 210	TOGGNANCCOGGCCOGCTCGCGCTCGT 367					12: pBCSK-, Site 1: HincII; 0.7-1.5 kb					lle, MD 20850, USA		Van Aken,S., Utterback,T., nn,M.A., Bedell,J.A., Rohlfing,T., t,D. and Lakey,N.	rte, Magnoliophyta, Lidpsida, Poales, Poaceae, PACCAD (coideae, Andropogoneae, Zea.
		COMMENT	JOURNAL	REFERENCE	ORGANISA	VERSION VERSION KEYWORDS SCURCE	DEFINITION	RESULT 13 CNS0091P	8	Q	₽ €	. 8	\$ 8	F 5	Matc	Query N	ORIGIN		mos	FEATURES	

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Path: New agnoscopic cas (1)

Determination of this Back-end sequence was carried out as part of a continuous that the Berkeley Drosophila Genome Project (Boss); and laboration with the Berkeley Brosophila Genome Project (Boss); and lanosates genome carried a power and an advantage of the Bossphila mation please see http://www.fraitity.org The BOSS brosophila mation please see http://www.fraitity.org The BOSS brosophila mation and the Bossphila Candid Genome and Library was repeated by Kanaroyo Genome and Candid Genome and Project and was considered by the BOSS brosophila BOS provided by the BOSS from the BOSS brosophila BOSS provided by the BOSS from the BOSS brosophila BOSS provided by the BOSS from the BOSS brosophila BOSS because arranged by the BOSS brosophila BOSS provided by the BOSS from the BOSS brosophila BOSS because arranged by the BOSS from the BOSS brosophila BOSS bro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Meoptera; Endopterygota; Diptera; Brathycera; Muscomorpha;
Rphydroidea, Drosophilidae; Drosophila,
(bases 1 to 925)
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Drosophila melanogaster
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AL053013
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Fax: 301-838-0208
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9712 Medical Center Drive, Rockville, MD 20850, USA
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/clone_lib="ZM_0.7_1.5 KB"
/note="Vector: pBCSK, 5 kte_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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811 MCTCCSTYBNBCYTSTSCGGSSSSSGKGGVTKCGCGGGGSSTNGMBGTSSACSSSS 867
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B188087 2-0C0842 Zebrafish shield stage whole embryo cDNA library
MPMGP637 Lamio rerio cDNA clone MPMGp637_2ZEI1.MPMSp637EI122 5',
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                                                                                                                                                                                                                                                                                                                     laboraty 123, dept.tehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-79, D-14195 Berlin, Germany
Tell: 449 30 8413 1612
Bax: 449 30 8413 1880
Bax: 449 30 8413 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark,M., Asmatad,P., Hennig,S., Johnson,S.L., and Lehtsch,H.
BST sequencing of exbratish shield stage cDNA library normalised
by oligonic jocycles Eingerprinting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii, Taleostei; Ostariophysi;
Cypriniformes; Opinidae; Danio.
1 (bases 1 to 738)
                                                                                                                                                                                                                                                        Email: hennis@molgen.mgg.de
5' EST sequencing of clones from a zebrafish shield stage library,
openalised from 55,000 starting clones by oligonucleotide
                                                                                                                                                                                                                 High quality sequence stop: 738
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/clone="BACR19D16"
/note="end : TET3"
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/clone wRWGp637_22E11,MRWGp637E1122"
(/clone wRWGp637_2E211,MRWGp637E1122"
(/clone type="whole embyy6 hrs post-fertilisation"
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/clone_lib="deviction" brief steage whole embyy6 cDNA
/clone_lib="deviction" brief steage whole embyy6 cDNA
                                                                                                                                                        /organism="Danio rerio"
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Pred. No. 4.5;
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Kirkness, E.F., Baina, V., Halpern, A.L., Levy, S., Remington, K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301-838-0200
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Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research
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GSS 27-S

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70

Matches Query Match

Local 631

Similarity

16.7%;

SOURCE KEYWORDS VERSION DEFINITION BI889087

Danio rerio (zebrafish) BI889087.1 GI:16096358 mRNA sequence. BI889087

ORGANISM

REFERENCE

Contact: Hennig S Unpublished (2001)

PEATURES

fingerprinting

G

Search completed: April 15, 2005, 17:41:36 Job time : 3303 secs

189 GTCGGCTCGGCGCTGGGGAACTCGGCCCCCGTCGGCGGGAAGTGGCCTCGGC 238

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

April 15, 2005, 17:44:42 ; Search time 514 Seconds (without alignments) 2915.326 Million cell updates/sec

Perfect score: Scoring table: 247 1 taggggaatccactccggag.....gtggcctcggcgtccgggga 247 IDENTITY NUC US-09-855-340B-6

Title:

Run on:

Total number of hits satisfying chosen parameters: Searched: 5622541 segs, 3033355566 residues

11245082

Gapop 10.0 , Gapext 1.0

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications NA:*

/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:* par 2-(phesias/) profession (1868, PBM, et al. et a 6/prodata/2/pubpna/US06_PUBCOMB.seq:* 6/prodata/2/pubpna/US07_NEW_PUB.seq:* 6/ptodata/2/pubpna/PCTUS 6/ptodata/2/pu 6/ptodata/2/pubpna/US08_NEW_PUB.seq:* 6/ptodata/2/pubpna/US11_NEW_PUB.seq:* 6/ptodata/2/pubpna/US60_NEW_PUB.seq:* 6/ptodata/2/pubpna/US09C_PUBCOMB.seq:* 6/ptodata/2/pubpna/US09B_PUBCOMB.seq:* bpna/US08_PUBCOMB.seq:* PUBCOMB. seq:* PUBCOMB.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution

SUMMARIES

No.	Score	Match	Score Match Length DB ID	8	ID	Description
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TITLE OF INVENTION	TITLE OF INVENTION:	TITLE OF INVENTION:	APPLICANT: Horan,		GENERAL INFORMATION:	Patent No. US20020076788AL	Sequence 6, Application US/09855340	US-09-855-340-6	RESULT 1
. BICS-SOCITION THOUSANCED		interior of processing of	Ann C.	dr., moude o.		76788A1	tion US/09855340		

TITLE OF INVENTION: Isolation of Micromomospora cathonacea var africa TITLE OF INVENTION: PMLPI integrate and use of integrating function TITLE OF INVENTION: after-specific integration into Micromomospora TITLE OF INVENTION: halophitica and Micromomospora Cathonacea Chromospora CURRENT APPLICATION NUMBER: US/09/855,340
CURRENT FILING DATE: 2001-05-15 FILE REFERENCE: INO1164K

SEQ ID NO 6 PRIOR FILING DATE: 2000-05-17 NUMBER OF SEQ ID NOS: 9 PRIOR APPLICATION NUMBER: 60/204,670 SOFTWARE: PatentIn Ver. 2.1

TYPE: DNA ORGANISM: Micromonospora carbonacea LENGTH: 247

US-09-855-340-6 Query Match Best Local Similarity 100.0%; Score 247; DB 9; ilarity 100.0%; Pred. No. 2.5e-63; Conservative 0, Mismatches 0; Length 247; Indels

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Matches 247; TAGGGGAATCCACTCCGGAGACGCCCGGAGCAATCCGGAGCATGACGGAGCAACCAG TAGGGGAATCCACTCCGGAGACGCCCGGGAGCAATCCCGGAGCATGACGGAGCAACCAG 0,

61 GTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCA

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                                                           NUMBER OF SEQ ID NOS: 9
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APPLICANT: Horan, Ann C.
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APPLICANT: Hosted, Jr., 7
APPLICANT: Horan, Ann C.
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; Pred. No. 7.9e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Sequence 17794, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-425-115-73105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 73105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Publication No. US20040214272A1
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LENGTH: 260
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CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: MRT4577_166671C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   concessacións as a capacidad de la concessación de la concessa de 
                                                                                                                                                                                                                                                                                                                                                                                                                         GTCGGCTCGGCGCTGGGCGACTCGGCCCCCTTCGGGGGAGTGGCCTCGGGCGTCCGGGG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCAATTNGGCCCCTGGCCCGGGGGGGGGGGGGGGTCCCGCGGGGCCCGGGCCCTGCGC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTGTTGACCCCCGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTCACCCGTAC 128
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100.0%; Fred. No. 4.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.0015;
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OTHER INFORMATION: Clone ID: PAT_MRT4530_23412C:1
US-10-437-963-17794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.0%;
nest Local Similarity 53.4%;
Matches 87; Conservation
                                                                                                                                                         US-10-425-115-31984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31984, Application US/10425115
Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 31984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhou, Yihna
APPLICANT: One, Younged
TITLE OF IMPARTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF IMPARTION: (021022)9
TITLE APPRENENCE: 1015/2223)9.
Best Local Similarity 48.
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
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                                                                                                                                                                                           OTHER INFORMATION: Clone ID: MRT4577_129183C.1
                                                                                                                                                                                                                                                                                LOCATION: (1)..(394)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 GGGGACTCGGCCCGTCGGCGGGGGAGTGGCCTCGGGGTCCGGGG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 ACTOGGAGGGGCCTTCGGCGTTCCTGAGGGTTCGGCGGTCGGCTCGGCGCTG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394
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Zhou, Yihua.
Cao.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cao,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yongwei
                                          16.84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
pred. No. 0.011;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 18; Length 1232;
pred. No. 0.0064;
                                                                                             DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                             Length 394;
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                                                                                                                                                                                                                                                                                                                           Sequence 42829, Application US/10369493 publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                        US-10-369-493-42829/c
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Publication No. U820040214272A1
GENERAL INFORMATION:
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 35614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleat Acid Molecules and Other Molecules Associative or Invention: Plants B File Reference 2-2(1922) E Plants B File Reference 2-2(1922) E Plants B File Reference 2-2(1922) E Plants E Plan
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                              APPLICANT: CAO, YOU
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                                  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR
                                                                                     APPLICANT:
                                                                                                                                                                                                            APPLICANT:
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110,

Indels

Gaps

Hinkle, Gregory J. Slater, Steven C. Goldman, Barry S. Chen, Xianfeng

Yongwei

211 CGGCCCCGTCGGCGGGGAGTGGCCTCGGCGTCCGG 244

534 desdendesdecedesdesdesdesdesdesdesdes 567

151 GGGGGCCTTCGGCGTTCCTGAGGGTTCGCGGTCAGGCGCTCGGCTCGGGGG 414 CGTCCAGGCGGAGCAGCACGGCCATGAGCGCCTCGGAGAACCGGGCCCGCTCGGCGCT 354 CGACGCGGCTCACGGCGCGCGCGCGCGCACGGCCGGGTAGCGCCCGGCA

CÓCCÓCOGACOÓCOTOCACOGTCTCCTÓCCOCCOGAGCACCCCCTCGAGCCGCCTCC

91 GCCCCGGTACGGGTTCAATTCCCCATCAGTCACCCGTACACGAAGGCCCCCTCCACTC 31 CANTOCOGRACIANOGRACIONACCAGORGATORACCOCOTORACCO

Conservative

0; Mismatches 108; Score 41.2; DB 18; Pred. No. 0.011;

> Indels Length 801; O; Gag

16.7%;

130 CÓCCÓCGGACÓCGTCCACÓGTCTCCCÓCCGCCCGAAGCAGCTCGAANCCGCGTCGC 151 GGGGGCCTTCGGCGTTCCTGAGGGTTCGCGGTCAGGCGGTCGGCGCTGGGGGAA

91 GCCCCGGTACGGGTTCAATTCCCCATCAGTCACCCGTACACGAAGGCCCCCTCCACTCGG 31 CANTCCGGAGCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAG

211 COGCCCGTCGGCGGGGAGTGGCCTCGGCGTCC 242 ,70 cáácarcacacacacacacacacacacacarac 39

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US-10-156-761-4150
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APPLICANT: SHIBA, TADAYOSHI
TITHE OF NUMBYTOSI: MASAHIBA
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Publication No. US20030119018A1
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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LOCATION: (1)...(1767)
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APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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 TITUS OF INVENTION: PLANTS WITH IMPROVED FILE REPERENCE: 38-10($2052)B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28
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Pred. No. 0.024;
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CURRENT PETICOTION INTERES: 185/1/156,761
CURRENT FILID DATE: 2000-05-20
FRIOR PRIVATE MATE: 2001-05-20
FRIOR PRIVATE: 2001-05-2
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CURRENT APPLICATION NEMBERS JP 0001-240689
BORDA APPLICATION NEMBERS JP 0001-240689
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Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SAKAKİ, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION. NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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SEQ ID NO 1
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APPLICANT: IKEDA, HARUO
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
LENGTH: 813
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Publication No. US20030119018A1
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HORIKAWA, HIROSHI
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53.1%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15; Length 9025608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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ORGANISM: Streptomyces avermitilis

TYPE: DNA

NAME/KEY: PEATURE

CDS

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US-10-156-761-5740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-156-761-3345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SUITAN. TADAYOSHI
APPLICANT: SAKSKI, YOSHIYKI
APPLICANTINI
APPLICANT: SAKSKI, YOSHIYKI
APPLICANTINI
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-156-761-3345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3345, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3345
LENGTH: 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP 2001-27269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1) .. (1212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 57.7%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 15.9%; Score 39.2; DB 15; Length 1212; Local Similarity 53.2%; Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 AGGCGGTCGGCCGTCGGCGCCCCCCCCCCCGCGGGGGAGTGGCCTCGGCGTCCG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 CÓCGGÁCGÁGGGCGCCGTCGÁGGTAÓTAGGGGCCTTCGGTCATCTCCTTCGTGAGGGTGC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 CGTACACGANGGCCCCCTCCACTCGGNGGGGGCCTTCCGGCGTTCCTGAGGGTTCGCGGTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 CGG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 GGG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Conservative
                                                                                                                                                                                                                                                                                                                                             641 GGCACCTCGÁCGCGTTCGÁGTACCTCAÁGCGCGAGAACAÁCCÁCTTCACGATCCÁCGCCG 700
                                                                      210 Toggoccogregacaga Aerea corcog corcog 245
                                                                                                                                                                      701 GÓGAGGCCTTCGGTCTTCCGTCGATCTGGCAGGCCCTCCAGTGGTGCGGCGGCCGACCGGC 760
                                                                                                                                                                                                                                                     150 AGGGGGCCTTCGGGGTTCCTGAGGGTTCGCGGTCAGGGGGTCGGCTCGGCGCTGGGGGAC 209
                                                                                                                                                                                                                                                                                                                                                                                                                            90 GGCCCCGGTACGGGTTCAATTCCCATCAGTCACCCGTACACGAAGGCCCCCTCCACTCGG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HORIKAWA, JUN
HORIKAWA, HIROSHI
TOGGTCACGGCGTGCGCATCATCGACGACATCCAGG 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKEDA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (813)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HARUO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
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4173750 GGCACCTCGÁCGCGTTCGÁGTACCTCAÁGCGCGAGAACAÁCACTTCACGATCCÁCGC

0; Gap

4173690 GGGAGGCCTTCGGTCTTCCGTCGATCTGGCAGGCCCTCCAGTGGTGCGGCGGCCGACCC 210 TOGGCCCGTCGGCGGAGTGGCCTCGGCGTCCGGG 245

150 AGGGGGCTTCGGCGTTCCTGAGGGTTCAGGGTCAGGCGGTCGGCTCGGCGCTTGGGG

US-10-437-963-30223/c

4173630 TCGGTCACGGCGTGCGCATCATCGACGACATCCAGG 4173595

Sequence 30223, Application US/10437963 publication No. US20040123343A1 GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.

Yihua

APPLICANT:

APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

Boukharov, Andrey A. Barbazuk, Brad Wu, Wei Cao, Yongwei Ping

SEQ ID NO 30223

TYPE: DNA

ENGTH: 512

NAME/KEY: unsure LOCATION: (1)...(ORGANISM: Oryza sativa

(512)

FEATURE: FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_34649C.1 OTHER INFORMATION: unsure at all n locations NUMBER OF SEQ ID NOS: 204966

TITLE OF INVENTION: Bice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTIONS 1,100 and Uses Thereof for Plant Improvement
FILE REFERENCE 10,10051,10
CURRENT APPLICATE NUMBER: USA/04/47/963
CURRENT FILE NUMBER: USA/04/47/963
CURRENT FILE NUMBER: USA/04/47/963

US-10-156-761-1/c

Sequence 1, Application US/10156761 Publication No. US20030119018A1

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US-10-156-761-1
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HATTOGI, MASAHIRA
TITLE DE INVESTICON: MOVEL DOLINOCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-29
FILOR APPLICATION NUMBER: US/2001-204089
FILOR APPLICATION NUMBER: US/2001-05-29
FILOR APPLICATION NUMBER: US/2001-05-29
FILOR APPLICATION NUMBER: US/2001-05-29
FILOR APPLICATION NUMBER: US/2001-07-276697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                          Matches 83; Conservative
                                                           Query Match 15.9%;
Best Local Similarity 53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-08-02
                                                                                                                                            OTHER INFORMATION: a, t, c, g, other or unknown
                                                                                                                                                                                                                            ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (4187715)
                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                           ENGTH: 9025608
90 GOCCCOGGTACGOGTTCAATTCCCATCAGTCACCCGTACACGAAGGCCCCCCTCCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
                                                  0; Mismatches
                                                                   Pred. No. 0
                                                                                         Score 39.2; DB 15;
                                                                        .019
                                                  73;
                                                                                             Length 9025608;
                                                       Indels
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US-10-437-963-30223

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Search completed: April 15, 2005, 19:10:14
Job time : 539 secs
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 69; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2082)
US-10-156-761-906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APLICANT: IKROÀ, MARIO
APPLICANT: IKROÀ, MARIO
APPLICANT: SELRA, UN
APPLICANT: SELRA, UN
APPLICANT: SELRA, TANAMORII
APPLICANT: SELRA, TANAMORII
APPLICANT: SELRA, TORINITALI
APPLICANT: SELRA, TORINITALI
APPLICANT: SELRA, TORINITALI
APPLICANT: SELRA, TORINITALI
CURBERT APPLICATION MORBER: UN/10/154,761
CURBERT FILHIO MARIE: 2007-0154,761
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JS-10-156-761-906/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 906, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.6%;
Best Local Similarity 46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OMURA, SATOSHI
                                                                                      347 G 347
                                                                                                                            243 G 243
                                                                                                                                                      407 CCGACGCCAGCTCGGTGCCGGGGACCACGGTCGCGTCGGGCCTGCGCGCCACGGTGTCC 348
                                                                                                                                                                                             467 CCCTCGNCGACGTCACCGTCGCCGGGGGATGATGTCGCCCGCCTCGCACACGACCAGGTCA 408
                                                                                                                                                                                                                                                                               123 CCGTACACGAAGGCCCCCCCCCCCGGAGGGGGCCTTCGGGCGTTCCTGAGGGTTCGCGGT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 GGTGTGGNNCNCGCCGTGGCAGCCGTCGNCGGCGGCGGGGGGATGGNGTCGTNGTCGNGGG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   412 ETECGTOCCÉCÉGÉNÉCÉGÉCEGÉCTECENCENTOTGETÉAGGGTENTCÓGTGNEGGÉGGAGGE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 CACGAAGGCCCCTCCACTCGGAGGGGGCCTTCGGCGTTCCTGAGGGTTCGCGGTCAGGC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 dikégikegréginkékécékkécégégékécégrecégécertécegegéégeérritintékégik 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 GGCCTGTTGACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTCACCCGTA 127
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                   15.3%; Score 37.8; DB 15; Length 2082; 57.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38.6; DB 18; Length 512,
Pred. No. 0.069;
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                              52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96; Indels
                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                          Gaps
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sequence 5, 1 sequence 5, 1 sequence 5, 1

Sequence 1408 Sequence

Sequence Sequence

sequence

Sequence Sequence Sequence Sequence Sequence

739 183

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OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summarios
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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11 //gpl.2 /pCodkes/1/ina/5A.COMB.seq;*
12 //gpl.2 /pCodkes/1/ina/5B.COMB.seq;*
23 //gpl.2 /pCodkes/1/ina/5B.COMS.seq;*
31 //gpl.2 /pCodkes/1/ina/5B.COMS.seq;*
41 //gpl.2 /pCodkes/1/ina/5B.COMS.seq;*
55 //gpl.2 /pCodkes/1/ina/backfiles1.seq;*
65 //gpl.2 /pCodkes/1/ina/backfiles1.seq;*
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Copyright (c) 1993 - 2005 Compugen Ltd
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4 US-09-02.540-662
2 4 US-09-902.540-662
65 3 US-09-103-840A-1
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2 4 US-09-94-016-1803
2 4 US-09-451-739H-1
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3 US-09-799-451-266
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sequence 30 Appl
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sequence 1903 Appl
sequence 1903 Appl
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Sequence 1, Appli
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Sequence 13134, A
Sequence 11907, A
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commence 523, App
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BROWN NO. 6314/ "APPLICATION US/0907340

BROWN NO. 100041100

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US-09-902-540-6674
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US-09-902-540-523
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Matches 67, Conservat
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PCT-1084-07799-5
US-09-949-016-1839
US-08-173-508-1
US-08-265-310-1
US-08-265-310-1
US-08-951-742-1
US-08-363-1244-1
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US-08-581-528A-5
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US-09-949-016-12165
US-09-949-016-13581
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pred. No. 0.16;
pred. No. 45; Indels
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SEQ ID NO 523

NUMBER OF SEQ ID NOS: 16825

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RESULT 4
US-09-949-016-11907
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Sequence 11907, Application US/09949016
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S-09-949-016-13134
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SEQ ID NO 13134
LENGTH: 31467
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US-09-902-540-523
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Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/337,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 69/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: YENTER, J. Craig et al. NOOMN GENES ASSOCIATED
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 67;
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Best Local Similarity 59.8%;
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LOCATION: (1)...(31467
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                                                                                          2768 CATCCTCCGCCCTGCGGCGGGGGGGGTGGGGTGGGCCGCAGGGCCAGGG 281
                                                                                                                                                                                                                                           2648 GCTCCTCGGTGACCTCGGGGCGTGTCCGGGAACCCGGCGGGGTGACCCCGGGGGGGAGG 2707
                                                                                                                             137 CCCCTCCACTCGGAGGGGGCCTTCGGCGTTCCTGAGGGTTCGCGGTCAGGCGGTCGGCTC 196
                                                                                                                                                                                                                                                                                                                          77 АСССССТБАССЬЮ ВССССОВТАСОВСТВОЛАТТСССАТСЬСТСАСССВТАСАСВЛАСВС 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2629 GAGCGCGGCGGTCCACCTTCCCGTTCGGCGTGAGCGGCAAGGCCTCCAGG 2680
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Similarity 48.0%;
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Pred. No. 0.58;
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Pred. No. 0.17;
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                                                                                                                                                                 SEQ ID NO 2
   OTHER.INFORMATION: GDC 1851
OTHER INFORMATION: ""P bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                  FEATURE:
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                                                                                                                                             LENGTH:
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US-09-103-840A-2
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US-09-949-016-11907
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                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                         APPLICAM: VENTER, John C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCHIOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local
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PRIOR PILME DATE: 2000-10-00
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILME DATE: 2000-09-08
PRIOR PILME DATE: 2000-09-08
SOFTMARE: PRICED for Mindows Version 4.0
SEQ_ID NO 11907012
ORGANISM: Mycobacterium tuberculosis
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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TITLE OF INVENTION: POLYMORITHESES IN EXCONS CENES ASSOCIATED
TITLE OF INVENTION: MITH HIMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                  DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VENTER, John C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robert D
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US-09-103-840A-1
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                                                       GENERAL INFORMATION:
                                                                  Seguence 266, Application US/09799451
Patent No. 6783969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPLICANT. VERTER, JOHN C.
REPLICANT. VERTER, JOHN C.
REQUERCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FLEISCHMAN, Robert D
APPLICANT: WHITE, Owen R.
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APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4411529
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48.6%; Pred. No. 4;
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Pred. No. 4;
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SEQ ID NO 266
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Best Local
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                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    Sequence 1, Application US/09410551B
Patent No. 6503737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids
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                                                    FILE REFERENCE: 30062-20026.00
CURRENT APPLICATION NUMBER: US/09/410,551B
CURRENT FILING DATE: 1999-10-01
                                                                                                                                                                                             APPLICANT: REEVES, CHRISTOPHER
APPLICANT: CHU, DANIEL
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                                 PRIOR APPLICATION NUMBER: US 60/139,650
                                                                                                                                                                                                                                  APPLICANT: KOSAN BIOSCIENCES,
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Wang, Jian-Rui
Ma, Yunging
Yamazaki, Victoria
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Wang, Zhiwei
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Pred. No. 1.2;
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JS-09-940-316B-1
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                                                                      Matches
                                                                                                      Query Match
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                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR FILING DATE: 199-06-17
PRIOR APPLICATION NUMBER: US 60/123,810
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/940,316B
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/410,551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09940316E
Patent No. 6759536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
                                                                                                                                                        LOCATION: (52275)...(71465)
                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                                                      ORGANISM: Streptomyces hygroscopicus
                                                                                                                                                                                                                                                                                                                                                    RIOR FILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PETICANT, MU, KAI
VETICANT, MU, KAI
VITLE OF INVENTION: CRESS CLUSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KOSAN BIOSCIENCES, Inc
                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/102,748
PRIOR FILING DATE: 1998-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (52275)...(71465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptomyces hygroscopicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/102,748
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123 CCGTACACGAAGGCCCCCTCCACTCCGACGGGGCCTTCCGGCGTTCCTGAGGGTTCGCGGT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30492 CGGSGCAGCGCGGGCCCGTCCGTGTACCCGGGCTCGGGCCAGACGGTCGGCGATGTCGTCG 3055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 GGG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 CCGTACACGAAGGCCCCCCCCCCCGGAGGGGGCCTTCGGGGTTCCTGAGGGTTCGCGGT 182
                                                                      69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 CAGGCGGTCGGCTCGGCGCTGGGGGACTCGGCCGTCGGCGGAGTGGCCTCGGCGTCC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHOSLA, CHAITAN
SANTI, DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REEVES, CHRISTOPHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHU, DANIEL
                                                                   Conservative
                                                                                     14.84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.8%;
                                                            Score 36.6; DB 4;
Pred. No. 2.3;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.6; DE
Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 77536;
                                                            54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Indels
                                                                                               Length 77536;
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                                                                                                                                                                             Matches
                        390 CTCTGGCGCGGCTCGGGCGGGGGGGGTCGTCCGGCGAGTCGTCGTCGTCGTCGGA 331
                                                        182 TCAGGCGGTCGGCTCGGCGCTGGGGGACTCGGCCCGTCGGCGGGAGTGGCCTCGGCGTC 241
242 CGGGGA 241
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US-U8-483-533-38
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                                                                                             Query Match
                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 38
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                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 11-APR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: U.STREET: Chicago
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                                                                           Watch 14.7%;
Local Similarity 55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                             NAME:
                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-MAR-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE
122 CCCGIACACGAAGGCCCCTCCACTCGGAGGGGGGCCTTCGGGCGTTCCTGAGGGTTCGCGG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30552 GGG 30554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30432 CCGTCGGCGAGGGCCACTTCCGGCCCAGACGGCGTCGTCGTCGTCGGCCCAGACGGCGCGCGGG 30491
                                                                70;
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                                                                                                                                                                                                                                                                                                                           Zeller, James P.
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    Application US/08483533
6172047

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                                                                Conservative
                                                                                                                                                                                                                                                     312/474-0448
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6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                   312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                      UNA (genomic)
                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                           31-MAR-92
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                                                                                                                                                                                                                                                                                                                                                                   07/861,233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for Treating Tumorigenic
                                                                                                                                                                                                                                                                                                                                                                                                            08/419,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/483,533
                                                                                                                                                                                                                                                                                                         28,491
                                                             0; Mismatches
                                                                        Pred. No. 1.
                                                                                                                                                                                                                                                                                             28097/32742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
                                                                                    DB 3;
                                                             56;
                                                                                    Length 1280;
                                                             Indels
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                                                       Gaps
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JS-09-283-471A-38
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US-09-283-471A-38/c
                                                                                                                                                                                                                                                  Query Match 14.7%; Score 36.4; Digest Local Similarity 55.6%; Pred. No. 1.3;
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INFORMATION FOR SEQ ID NO: 38:
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                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/483,533
PILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 31-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TELEPHONE: 312/474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TILE OF INVENTION: Method For Treating Tumorigenic Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/419,853
FILING DATE: 11-APR-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                             242 OGGGGA 247
                                                                              390 CTCTGGCGCGGGTCGGGGGGGGGGGTCTCCGGCCAGTCGTCGTCATCGTCGTCGTCGGA 331
                                                                                                                                                    122 CCCGTACACGAAGGCCCCCTCCACTCGGAGGGGGCCTTCGGCGTTCCTGAGGGTTCGCGG 181
                                                                                                                                                                                                                                   70;
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6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                           1280 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312/474-0448
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                                                                                                                                                                                                                                   conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roizman, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                DNA (genomic)
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                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                      DB 3; Length 1280;
                                                                                                                                                                                                                                   56; Indels
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Best Local Similarity
Thehes 70; Conservat
                                                      US-09-283-471A-39/c
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GENERAL INFORMATION:
                                   Sequence 39, Application US/092834718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6172047
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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55.6%; Pred. No. 1.
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28097/32742

Mismatches

DB 3; Length 1300; Indels 0 Gaps

Matches

330 CGCGGA 325

Query Match

NUMBER OF SEQUENCES:

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US-08-483-533-36/c
                                                                                                                                                                                                                                                                                             RESULT 14
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                                                                                                                                                                                     Sequence 36, Application US/08483533
Patent No. 6172047
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.7%; Score 36.4; DB 3; Length 1300;
Best Local Similarity 55.6%; Pred. No.1.3;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
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CITY: Chicago
CITYE: Illinois
United
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/861,233
PILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA
APPLICATION NUMBER: 08/419,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floopy disk
COMPUTER: IN PC COMPAILING
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: FatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAYA:
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MEDIUM TYPE: Floppy
                                                                                        APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method for Treating Tumorigenic
TITLE OF INVENTION: Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 27.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 11-ARR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/483,533
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                            CORRESPONDENCE ADDRESS:
                                                                         NUMBER OF SEQUENCES:
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STRANDEDNESS: single
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FILING DATE: 04-APR-1999
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STREET: 6300 Sears Tower, 233 South Wacker Drive
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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4448	CILII CHICAGO STATE: Illinois COUNTRY: United States of America	PONDENCE ADDRESS ESSEE: Marshall ET: 6300 Sears	Chou, Jos NVENTION: SEQUENCES:	55.	RBSULT 15 08-09-281-471A-36/c ; Sequence 56, Application US/09283471A	350 COCCGA 345		182 TENGGEOGREGOETEGGEOGTEGGGGGETEGGGCCCCCTCGGGGGGGGTGGGGCTCGGGCTCGGGCGGG	122 CCCGTALACABAGECCCCTCALTCGAAGGGGCCTTCGGGGTCCTGAAGGTTCCTGAAGGTCCGGG 18:	Query Mach 14.7k; Score 5.6; BB 3; Length 1327; Rest Local Similarity 5.6k; Fred. No. 1.3; Rest Local Conservative 0; Mismatches 56; Indels 0; Gaps (Mismatches 70; Conservative 0; Mismatches 56; Indels 0; Gaps (Mismatches 56; Indels 0; Gaps (Mismat	COUNTRY: Intitled States of America ZET GOOG-SATE ZET GOO	CITY: Chicago

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Query Match 14.7%; Score 36.4, DB 3, Length 1327, Best Local Similarity 55.6%; Pred. No. 1.3; Matches 70; Conservative 0, Mismatches 56; Indels 0
                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1
MOLECULE TYPE:
-09-283-471A-36
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SEQUENCE CHARACTERISTICS:
LENGTH: 1327 base pairs
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APPLICATION NUMBER: 07/861,233
FILING DATE: 31-MAR-1992
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TELEPHONE: 312/474-6300
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/283,471A
FILING DATE: 04-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Zeller, James P.
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/419,853
                                                                                                                                                      122 CCCGTACACGAAGGCCCCCTCCACTCGGAGGGGGCCTTCGGCGTTCCTGAGGGTTCGCGG 181
350 CGCGGA 345
                                      242 CGGGGA 247
                                                                         182 TCAGGCGGTCGGCGCTCGGCGCGCGCCCCGTCGGCGGGAGTGGCCTCGGCGTC 241
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Search completed: April 15, 2005, 17:44:29 Job time : 160 secs

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using sw model	GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Sequence 45, Sequence 1,

579

Scoring table:	Title: US-09- Perfect score: 1179 Sequence: 1 gtgt
scoring table: IDENTITY_NUC	US-09-855-340B-1 1179 1 gtgtggatcgagaagaacggtgttggccgacgcagcatga

Run on:

April 15, 2005, 19:01:23 ; Search tene 971.841 Seconds (without alignments) 8204.076 Million cell updates/sec

Sequence

Sequence

Sequence 106

Sequence 115, Sequence 115 Sequence 34,

Total number of hits satisfying chosen parameters: Searched: 5622541 seqs, 3033355566 residues 11245082

Gapop 10.0', Gapext 1.0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 10 100

Database Published Applications NA:* Listing first 45 summaries

21:	20:	19:	18:	17:	16:	15:	14:	13:	12:	11:	10:	9:	80	7:	6.	5	4.	3:	2:	1	Tony
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pred. No. is the number of results predicted by chance to have score greater than or equal to the acore of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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Sequence Sequence Sequence Sequence Sequence

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Sequence Sequence Sequence

Sequence

APPLICAL APPLICANT: HORAN, AN TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: IN01164K
CURRENT APPLICATION NUMBER: US/09/855,340
CURRENT FILING DATE: 2001-05-15 pMIP1 integrase and use of integrating function site-specific integration into Micromonospora halophitica and Micromonospora carbonacea chromo 2001-05-15 var africa

PRIOS PILMES DATE: 2001-55-17 MINESE OF ESC. DE NOS: 9 SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 1 LENGTH: 1179 TYER: DNA ORGANISM: Micromonospora carbonacea G.G.9-855-140-1

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GACGAGGAGCTGACGGACGTGTTGGCCGACGCAGCATGA 1179
                         GACGAGGAGCTGACGGACGTGTTTGGCCGACGCAGCATGA 1179
                                                                 CTCGCGGCGATCGAGGAGGCGATGGCGGGCTCCGGGCTGAGGACCTGGAGGCGGAACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTROL TO THE PROPERTY OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACGGCCTGCTGCACACGATCTGCGGCGGCGGCGATCGCGGCGAAACGGATCAGGCTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCCGGAGTCCACGCGGGGTCGTCGGAAGCCGCTGGCAGCGAAGACGATCAGCAACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCCGGNGTCCACGCGGGGTCGTCGGAAGCCGCTGGCAGCGAAGACGGATCAGCAACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGAGGCCGGCGTCGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGAGGCCGGCGTCGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGGNGGGCAACCGGATGCGCAACCACCTCCTGCCCATACTCGGCCATCTCACCCTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOSGAGGGCAACCGGAATCCGCAACCTCCTGCCCATACTCGGCCATCTCACCCTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTGCGGAGCAGTTGCAGGGCAAACGCGCTCATGCCGCGCGGGGGGTCAGATTACCCTCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCCAGTCGCCGAAGACCGCGAAGGGCCGGCGCACGGTCAGTTTCACC
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120 60 60 0

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541 541 481 481 421 421 361 361 301 301 243 241 181 181

601 CTOSTOSCGACCOGTCTGAGGTGGGGTGAGGCGATCGGCCTGCGCGGGCCGGGTCGAC

660 600 540 48 480 420 420 360 360 300 300 240 240

cceanantcertceerrancaceecricecccccacacreecaccecricercarecre CCGGAGATCGGTCGGCTTATCACGGGGGCTTCCGGCGGCACTGGGGAGACCGCTCGTCATGCTG CCGTGCTCTTCGACGATGCTGCCCCGGCGCGAGGCGAAAGAGATGAAGTTCCTGAGCGAC CACGGCCTGCTGCACACGGATCTGCGGCGGCGGCGATCGGCGGAAACGGATCAGGCTCAAC CACGGCCTGCTGCACACGATCTGCGGGGGGGGGATCGGCGGAAAACGGATCAGGCTCAAC CCGTGCTCTTCGACGATGCTGCCCCGGCGCGAGCCGAAAGAGATGAAGTTCCTGAGCGAC 540

TOGCCGGAGTCCACGCGGGGTCGTCGGAAGCCGCTGGCAGCGAAGACGATCAGCAACTGC GAGCTGGACGGCCAGCCCAGCAGTGGGTCAACCACCTGGACGCCGGCGTCGGCCCC GAGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGAGGCCGGCGTCGGCCCG TOGGAGGGCAACCGGATCCGCAACCACCTCCTGCCCATACTCGGCCATCTCACCCTTGAC TCGGAGGGCAACCGGATCCGCAACCACCTCCTGCCCATACTCGGCCCATCTCACCCTTGAC

TGGCCGGAGTCCACGCGGGTCGTCGGAAGCCGCTGGCAGCGAAGACGATCAGCAACTGC

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APULZANT; Henied, Thomas J.
APPLICANT; Henied, Thomas J.
APPLICANT; Henied, Thomas J.
APPLICANT; Henied, Thomas J.
APPLICANT; Henied, 
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US-09-758-759-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.7%; Score 1176; DB 11; Best Local Similarity 100.0%; Pred. No. 1e-301; Matches 1176; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 176, Application US/09758759
Publication No. US20040101832A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEY: CDS
LOCATION: (1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Micromonospora carbonacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                              121
                                                                                                                                                      121
                                                                                                                                                                                                                           61 GTCACCATTCAGACCGGTTATCCGACGAAGAACCAGCGCCAAGAATGCGATGGTGCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTSTGGATCGAGAAGAACGGGCCCGTCTACCGCATTCGGGGACCTCGTTCGCGGGTAAAAAG
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CGTGCGGAGCAGTTGCAGGGCAACGCCCTCATGCCGGCGGCGGTCAGATTACCCTCGCC 180
                                                                                            GTCACCATTCAGACCGGTTATCCGACGAAGACCAGCGCCAAGAATGCGATGGTGCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGTGGATCGAGAACGGGCCCGTCTACCGCATTCGGGGACCTCGTTCGCGGTAAAAAG
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CTGGTGGCGACCGGTCTGAGGTGGGGTGAGGCGATCGGCCTGC

us-09-855-340b-1.rnpb	b-1.rnpb
	0 3
CHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Qy 393 GCTGGCAAGGAAGACGATCAGCAACTGCCACGGCCTGCTGCACACGATCTGCGGGCGCG
CAGGAGCTGGCCAGCACG 720	Db 390 daridadahaccchcddrattchhaddcthacchacttacthacact
CAGGAGCTGGCCAGCACG 720	Oy 453 GATCGCCGCARACCGCARCCCCGARCCCGGACCCGGACCAGACCGCACAGCTCACCCGGACCGACCGGACCGACCGACCGACCGCGACCGACCGACCGACCGACCGACCGACCGACCGACCGACCGACCGACCGACCGACCACACCAC
AAAAGTGACGACGTCGTG 840	Db 510 CGTGCCTGAGCGGCCTGTTTTGTCGGTGGGGGAAGICTTTGACGTCGAGTGAGGTGAG
	GOOGACTGGGGACCGCTCGTCATGCTGCTTGGGGGACCACCTTCGGGGACCGTTCGGGTATGCTCCTTGGGTGGG
	633
COCCOCATCIOSOTCARG 900	
CIGCGGCACACICACGCG 960	693
CGCCGCCTCGGTCACTCG 1020	Db 681 COGCOGGCACAGGCCGAGTTGCAGAACGGCCCCTTTCGACAAGGCGCCCCAAGTCG
CGCCGCCTCGCTCACTCG 1020	Qy 753 GAAGGGCCGGCGCACGGTCAGTTTCACCACGAAAGTCGCTCTACTGCTTACCACCACTCTCTCT
GAGGTCGACGAGGGGATC 1080	Db 741 CGCGGGCCTTCGAACCGTTTCCTTCCCCGCTGAACCGCGGGAAACGCGGG
	Qy 813CCCCCCAAAGAAAGAAAGAAAGAACCTGTTCGTTCGTCCACAGGGTGGG
STACCIGGAGGGGGAACTC 1140	864
	Db 861 GCTTCGGCGGAGCAACTTCCGGGATGACTCAAGGCCAGGAAGGCAGCGGGGGT
	Db 921 GCCCAAGCTGCACTTTCACGACCTGAGGCATAC 953
	RESULT 4 US-10-156-761-1/C
	0222
	ISHIKAN HORIKAN SHIBA, SAKAKI, HATTOR
	TILLE UPERMICE: 249-262 OTHER METERICATION NUMBER: UP/10/156,761 OTHERWY TILMO DATE: 2002-05-29 PRICE APPLICATION MADRER: UP 2001-204099
,	PAZOR FILING DATE: 2001-05-30 PAZOR FILING DATE: 2001-05-30 PAZOR FILING DATE: 2001-08-02 NUMBER OF SEQ ID NOS: 15:109 NUMBER OF SEQ ID NOS: 15:109
	SEQ ID NO 1 LENGTH: 9025608
	ORGANIAM: Streptomyces avermitilis FEATURE:
Length 1137;	NAME/KEY: m.sc reature LOCATION: (4187115) COTHER INFORMATION: a, t, c, g, other or unknown
	IIS-10-156-761-1

US-10-156-761-3714

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO

APPLICANT: APPLICANT:

ISHIKAWA, JUN HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYÖSHI APPLICANT: SAKAKI, YOSHIYUKI APPLICANT: HATTORI, MASAHITAK TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

Sequence 3714, Application US/10156761 Publication No. US20030119018A1

1141 GACGAGGAGCTGACGGACGTGTTGGCCGACGCAGCA 1176

GACGAGGAGCTGACGGACGTGTTTGGCCGACGCAGCA 1176

1021 TCGATCGCGGTCACGGATCTGCTGTACGGGCACCTGCGTGAG

CTCGCGGCGATCGAGGAGGCGATGGCCGGCGTCCGGGCTGAG TOGATOGOGGTCACGGATOTGCTGTACGGGCACCTGCGTGAG GCGATCCTGATTTCTGCCGGGGGGGGTCCGCTGTCGGCGATCTCC GCGATCCTGATTTCTGCCGGGGGTCCGCTGTCGGCGATCTCC GCGTGCGAGGAAGCCGGGCTTCCGGGCTTACGCATTCACGATY GCCTGCGAGGAAGCCGGGCTTCCGGGCTTACGCATTCACGATY TTCACCGCGCGAAAGGCGGGATGGTAAGGACGCGCAATTTCC ACGAAAGTCGCTCTACTGCTTACGCCACTCATCGCCGGAAAG ACGAMAGTCGCTCTACTGCTTACGCCACTCATGGCCGGAAAGA

CTCGCGGCGATCGAGGAGGCGATGGCCGGCGTCCGGGCTGAG

961 961 901 901

1081 1081 1021

; NAME/KEY: CDS ; LOCATION: (1). US-10-156-761-3714

.. (1137)

FEATURE: LENGTH: 1137

Ouery Match 5.
Best Local Similarity 48.
Matches 280; Conservative

48.9%;

Score 65.8; DB 15; pred. No. 1.3e-07; 0; Mismatches 272;

Length 1137; Indels

US-10-156-761-1 Query Match

5.6%; ņ ú Score 65.8; other or unknown DB 15;

Length 9025608;

Gaps

SEQ ID NO 3714

TYPE: DNA ORGANISM: Streptomyces avermitilis NUMBER OF SEQ ID NOS: 15109

PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-98-02 FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089 Ş

841 841 783 781 721 721

TTCACCGCGCGAAAGGCGGGATGGTAAGGACGCGCAATTTCC

S

661 601

CTGCTCGCCGCGCCCCGGCTGACCGTCGTCGAGCAGCTCC CTGCTCGCCGCGCGGCCCGGCTGACCGTCGTCGAGCAGCTCC

GGAGAGCTCGTCTTCCAGTCGCCGAAGACCGGCGAAGGGCCGGC GGAGAGCTCGTCTTCCAGTCGCCGAAGACCGCGAAGGGCCGGC

Best Local Similarity

48.91;

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US-10-369-493-43111
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                           Query Match
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 43111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43111, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hished "Group,"
APPLICANT: Slates, Strong C.
APPLICANT: Slates, Strong C.
APPLICANT: Slates, Strong C.
APPLICANT: Slates, Strong C.
APPLICANT: SALESSAME STRONG C.
APPLICANT SLATES C.
APPLICANT SLATES C.
APPLICATION: FLATES C.
APPLICATION: STRONG C.
APPLICATION: ST
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                             OTHER INFORMATION: unsure at all n locations
                                                                                                                                                            LOCATION: (1) .. (1743)
                                                                                                                                                                                              NAME/KEY: unsure
                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                     ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4615021 GCCCAAGCTGCACTTTCACGACCTGAGGCATAC 4614989
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                                                                                                                                                                                                                                                                                                                                       1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  924 GGGCT---TACGCATTCACGATCTGCGGCACAC 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   633 GATCGGCCTGCGGCCGGGCCGGGTCGACCTGCTCGCCGGCGGGCCCCGGCTGACCGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTCGGCGGAGCHACTTCCGGGATGACTGGATCHAGGCCAGGAAGGCAGCGGGCGGCTCTC 4615022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGGGCCTTCGAACCGTTTCCTTCCCCGCTGAGCTGGTCGACGAGATCAGCCACCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COGCOGGCACAGGCCGAGTTGCAGAACGGGCGGCTCTTCGACAAGGGGGCCCAAGTCGGC 4615202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CGCCGGAAAGAAAAGTGACGAGGTGGTGTTCACCGCGCGAAAGGGCGGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCCGCGCTGCGTCGCAAGGACATCGATCTGAACGGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCGCGCTACCGGCTGCTCGTCCTCGGCTGCGTTCACGACTCTCCGGCTTCGGCGAGCT 4615313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGCACTGGGGACCGCTCCTCATGCTGGTGGTGGGGACCGGTCTGAGGTGGGGTGAGGC 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTGCCTGAGCGGCCTGTTTTGTCGGTGGCGGAAGTCTTTGGCGTCGCCTATGCCATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTAGATGACGÁGCTGÁŤCCGCCGCÁÁCCCGTGCCGGATCAAAGGCGCGGACAGTTACGÁ 461543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGGGGGAGCCCACGGTGGTCNAGGCGTACCNACTGCTGCGGGGCCCTGATGAACACCGGC 4615493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATTOGCGGCGAAAACGGATCAGGCTCAACGCGTGCTCTTCGACGATGCTGCCCCGGGCGCGA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                    4.9%;
Score 57.2; DB 17; Length 1743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.5e-07;
0; Mismatches 272; Indels
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                                                                                                                                                                                                                                                            Matches 262;
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Micromonospora rosaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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AGGTCGTCGCCCTGGTCGAGGCCATCAACCCGGGCTACCGGACGGCGGTCCTGATCGCGG 616

Local Similarity

Conservative 46.24;

0; Mismatches 299; Score 56.6; DB 9; Pred. No. 3.5e-05;

Length 1161 Indels

6

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US-09-821-167-15
SEQ ID NO 15
                                                                                                                              FILE REFERENCE: IN011490
CURRENT APPLICATION NUMBER: US/09/821,167
CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09821167
Patent No. US20020015989A1
                                               PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                   APPLICANT: Noram, Ann C.
ITILE OF INVENTION: Isolated Nucleic Acids from Micromonospora rosaria
TITLE OF INVENTION: plasmid pMR2 and Vectors Made Therefrom
                     SOFTWARE: Patentin Ver. 2.1
                                                                                               PRIOR APPLICATION NUMBER: US 60/194,461
                                                                                                                                                                                                                                                             APPLICANT: Hosted Jr., Thomas J.
APPLICANT: Horan, Ann C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1597 ACGCGCCGCGCGCTGTGCGCCACGTTGAAGGGGGGGCGCGCTCGACCAGGAGCTCGAGCGC 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            718 АССЕВАВАССТССТСТТССВСТСССВАВСАССССТВАВСЕСТВАВССССТВЕТ 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                658 GACCTGCTCGCCGCGGCGCCCGGCTGACCGTCGTCGAGCAGCTCCCAGGAGCTCGCCAGC 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCGGGTGGCGATGACGCAGCTCTACGCACTGGACGCCATCCCCGGGGGCCTACGACAGG 1596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCCGTGCTCTTCGACGATGCTGCCCCCGCGCGCGAAAGACAAGAAGAAGATGAAGTTCCTGAGC 537
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US-09-821-167-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09821167
Patent No. US20020015989A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Isolated Nucleic Acids from Microemonopoca romaria
TITLE OF INVENTION: plannid pMR2 and Vectors Made Therefrom
FILE REFERENCE: INVISAGO: USO/9621,167
CHESENT REPLICATION MAGENT. 200-103-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hosted Jr., Thomas J. APPLICANT: Horan, Ann C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
Matches
                                         Best
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/194,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Micromonospora rosaria
                                                                                                                                                                                                                                              NAME/KEY: RBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     914 GGGGAAAGGTCGGACTCGACACCTCACCTTCCACGACCTGCGGCACACCGGTCAGACCC 973
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al Similarity 46.2
262; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGTOGTACCOGTÓATCCGCCTGCACCTCGACGAGTTCGCCGGGAAGGÁTCGCCTÓTTCG 853
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (6391) . (6394)
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                                                                                                                                                                                                                                                                               (9834) . . (9837)
                                         46.24
        Score 56.6; DB 9;
pred. No. 3.6e-05;
0; Mismatches 299;
                                                                                                  Length 11188;
                        6
                                Gaps
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545 AGATCGGCTTATCACGGCGCTCCGGCACTGGCGACCGCTCGTCATGCTGCTGG 604

Mismatches 102;

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US-10-156-761-3695
                                                                                         NAME/KEY: CDS
; LOCATION: (1)..(1179)
US-10-156-761-3695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3695, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3695
LENGTH: 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
Query Match
Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OMURA,
APPLICANT: IKEDI
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                              ORGANISM: Streptomyces avermitilis
                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    785 ААСТСОСТСТАСТОСТАСОССАСТСАТСОССОМАМАВААНОТОВАСОНОСТОТОТ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HORIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SATOSHI
                            4.7%; Score 55.8; DB 15;
53.4%; Pred. No. 5.7e-05;
                  Indels
                                                             Length 1179;
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) ORGANISM: Streptomyces noursei ATCC 11455
US-10-203-295-2
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NUMBER OF SEQ ID NOS: 49
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PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: GB 0008786.6
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CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: POT/GB 01/00509
PRIOR FILING DATE: 2001-02-08
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APPLICANT:
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Publication No. US20040115762A1
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FILE REFERENCE: 1181-265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                     4471 GGTGAACGAČGTGCAĞGAĞGTĞCAĞAAČCTCGCCCAĞACCGGCTTCGGCATCGTCGTCTĞ 4412
                                                                                                                                               4591 GGCCGCCCGGACCGCGACGGCGATGGGGCGCGATCTGCGGTCCGGCGCTCTTCCGCCGCAT 4532
        537 CGACCCGGAGATCGGTCGGCTTATCACGGCGCTTCCGCCGCACTGG---CGACCGCTCGT 593
                                                                                             477 СААССОВТВЕТСТТСВАСВАТВСТВССССВВЕВСВАВССВАВАВАВАТВАВТТССТВАВ 536
                                                                                                                                                                                                                                                                            357 сесотвассоваютселсвоваютсятервальное световеля святольного дела да в
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                                                                                                                                                                                       ствесь, свесстветьсь сватуственного свесовтов свесов свать пределение статем.
                                                                                                                                                                                                                                                                                                                         CGCCACGCTACTGACCGCGGCCGGCGTCGCGCGGGGTCATCATGAAAATCCTCGGGGA 1037
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Sekurova, Olga Nikalayivna
Fjaervik, Epsen
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Sletta, Havard
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Valla, Svein
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.84;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55.8; DB 18;
Pred. No. 6e-05;
0; Mismatches 417;
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Query Match
Best Local Similarity
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US-10-203-295-35
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                                                                                                                                                                                 SEQ ID NO 35
                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: GB 0009387.2
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PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: GB 0002840.7
PRIOR PILING DATE: 2000-02-08
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CURRENT APPLICATION NUMBER: US/10/203,295
CURRENT FILING DATE: 2003-07-79
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Publication No
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TITLE OF INVESTION: Novel genes encoding a nystatin polyketide synthase and their
TITLE OF INVESTION: manipulation and utility
                  ORGANISM: Streptomyces noursei ATCC 11455
                                                                                             TYPE: DNA
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                                                                                                                                  125401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zotchev, Sergey Borisovich
Sekurova, Olga Nikalayivna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTCGGTCACTCGTCGATCGCGGTCACGGATCTGCTGTACGGGCACCTGCGT 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGACGAGGTCGTGTTCACCGCGCGAAAAGGCGGGGATGGTAAGGACGCGCAATTTCCGGCG 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sletta, Havard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ellingsen, Trond Erling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strom, Arne Reider
Valla, Svein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fjaervik, Epsen
Brautaset, Trygve
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44.81;

Score 55.8; DB 18; Pred. No. 6.1e-05;

Length 125401

Matches

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US-10-260-238-5339/c
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   Sequence 5339, Application US/10260238
Publication No. US20040016025Al
                                     APPLICANT:
                                                                                                   APPLICANT:
                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                 APPLICANT: Budworth, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGCGGGCCCGGTCTGTGCCGGCCGGATCGCGGAGGTCCTGGACACCGGGT 3879
                                                                                                                                                          Cooper, Bret
                                                                                                                                                                                                                        Moughamer, Todd
                                     Kreps, Joel
                                                                          Katagiri
                                                                                            Glazebrook, Jane
Goff, Stephen A.
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US-10-260-238-5339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRENT PAPALCHYTON MANSER: US/10/560,238
CORRENT FILING MARTE: 2002-079-8
PRICE PAPALCHYTON MANSER: US 60/35,48
PRICE PALICHYTON MANSER: US 60/35,48
PRICE PILING DAME: 2001-07-8
PRICE PILING DAME: 2001-07-8
PRICE PILING DAME: 2001-07-8
PRICE PILING DAME: 2003-04-04
AMMERIC OF EAST DAME: 4003-04-04
AMMERIC OF EAST DAME: 4003-04-04
AMMERIC OF EAST DAME: 4003-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5080, Application US/10156761
.; publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-156-761-5080
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LENGTH: 846
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Matches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                              APPLICANT: ONURA, SATOSHI
APPLICANT: IXEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                       APPLICANT SHIBA, TADAYOGHI
APPLICANT SHORY VOSHIUNI
APPLICANT SHORY VOSHIUNI
TITIGA OF HAVBATTON AVASAMISA
APPLICANT HAVBATTON AVASAMISA
APPLICANT AVASAMISA
COURSENT PATALONTON HAMBER 10/10/156,761
CURRENT PATALONTON HAMBER 10/10/156,761
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489 TTCGACGATGCTGCCCCGGCGCGAGCCGAAAGAAAAAATTGAAGTGCTGAGCGACCCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTCTTCCA 737
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Pred. No. 0.00013;
0; Mismatches 197;
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Indels Length 846; 0 Gap

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APPLICANT:

Provart, Nicholas Ricke, Darrell

2001-272697

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CURRENT PAPLICATION NUMBER: US/11/762.107
CURRENT FILING DATE: 2006-01-20
PRIOR PAPLICATION NUMBER: USEN 66/441.126
PRIOR PELING DATE: 2001-01-21
PRIOR PELING DATE: 2001-01-20
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Publication No. US20050043297A1
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APPLICANT: Bachamun, Brian
APPLICANT: Pixaes, Mahmod
TITLE OF INVESTION: A PRANSKYL DIBENZODIAZEFINONE, PROCESSES FOR ITS PRODUCTION AND
TITLE OF INVESTION: A PRANSKYLDIAZEFINONE, PROCESSES FOR ITS PRODUCTION AND
TITLE OF INVESTION: A PRANSKYLDTICAL
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Best Local Similarity
Matches 227; Conserv
                              NUMBER OF SEQ ID NOS: 85
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NAME/KEY: CDS
LOCATION: (1).
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Pred. No. 0.00022;
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                                                                                                              TITLE OF INVESTIGN FAMISSIC DISBROGATICAL

TITLE OF INVESTIGN A PREMANCIFICAL

THE RETERENCE: 1005-1018

CHEMICAL PROPERTY ON A PREMANCIFICAL

THE RETERENCE: 1005-1018

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Publication No. US20050043297A1
SEQ ID NO 1
                                                                                          NUMBER OF SEQ ID NOS: 89
                                        SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Farnet, Chris
APPLICANT: MCAlpine, James
APPLICANT: Zazopolios, Emmanuel
APPLICANT: Bachmann, Brian
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PROCESSES FOR ITS PRODUCTION AND ITS

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; ORGANISM: Micromonospora sp. strain 046-ECO11
US-10-762-107-45
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SEQ ID NO 45
LENGTH: 1104
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GACTCGCAGGGGAAGTCCCCCCCTCGTCACAGTGG 87
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                                                                                                            CCGCCGCACTGGCGACCGCTCGTCATGCTGCTGG 604
                                                                                                                                                                                                                        GCCGGCGGGCGGACCAACTACCTCAGCGAGCTGGTCTCCGGCGGCGGGGGCGGGTGCTCGCCGTG
                                                                                                                                                                                                                                                                                                                                                GCGATCGCGGCGAAAACGGATCAGCCTCAACCCGTGCTCTTCGACGATGCTGCCCCGGGCGC 510
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Pred. No. 0.00028;
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ORGANISM: Micromonospora sp. strain 046-ECO11
US-10-762-107-1
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Publication No. US20030119018A1
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                                                                                                                                SEQ ID NO 5794
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APPLICANT: SAKAKI, YOSHITURA
APPLICANT: MATORIA (MARITURA
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
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                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JF 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OMURA, SATOSHI
                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1510
                                             TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                                           LENGIH: 426
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Pred. No. 0.00029;
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search completed: April 15, 2005, 22:50:53 Job time : 891.841 secs

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1071 CGAGGGGATCCTCGCGGCGATCGAGGAGGCGAT 1103

354 CCACCAGATCGCCGACTACGTCGACGGTCAGAT 386

1011 CGGTCACTCGTCGATCGCGGTCACGGATCTGCTGTACGGGCACCTGCGTGAGGAGGTC

GGGCCACTCCTCCGTGCGGGCCGCG---CTGATCTACCAGCACCTCGTCAACGGCCGT

237 CACCOGGAACACGCTGCCACCGGCGGCGCCACCACCGCGAGCTGATGCACCGC 951 CACTCACGCGGGGATCCTGATTTCTGCCGGGGGCGTCCGCTGTCGGCGATCTCCCGGCGC

NAME/KEY: CDS

FEATURE:

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Matches 142; Conserv
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177 CTGGCTCCGAGCGCTCGACCGGGTCTCGGTGACGTCCATTTCCACGATCTCCGG
                                                                              831 CGAGGTCGTGTTCACCGCGCGCAAAQGCGGGATGGTAAGGACGCGCAATTTCCGGCGG
                                   891 CTGGGTCANGGCGTGCGAGGAAGCCGGGCTTCCGGGCTTACGCATTCACGATCTGCGG
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Qy 497 TGCTGCCCCGGCGCGAGGCGAAAGAGATGAAGTTCCTGAG	99	Seguence	2 1513 4		26 49	
Db 1167 CGCCGTCCCCCGATACTTGTCCACCAACCCTGCGTCGGGC	0	US-09-902-540-5454 Sequence 5975, Ap	44	9.8	24	
Oy 437 CSATICIBCIGGUSCOGCUSTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2 >	05 Sequence	3 3372 4 0	0.2	c 23 50.	
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оу 377 сесстостоскальстоствесь се в доли в при в	, 0	4 Sequence 114	٠.	51.4	18 51.4	
Db 1055 ACATCGCCCGCTGGGTGAAGGTCATGGAAACCACCGGGGG		Sequence 34,	44	51.4	16	
Qy 317 TCACCCAGCAGTAGTCAACGACCTGGAGGCGGGGTCGGG		Sequence	516 4 U	44	14 51.4	
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Qy - 257 TCCGCAACCACCTCCTGCCCATACTCGGCCATCTCACCCTT		US-09-902-540-6567 Sequence 6567, AF			10 . 52.8	
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llarity 48.5%;		US-09-821-167-1 Sequence 1, Appril	11188 4	4.	7 56.6	
5.2%; Score 61.		Sequence	1161 4	6.6 4.8	6 56	
US-09-269-717-16		US-09-902-540-5392 Sequence 5394, Ap	4719 4	57	4	
: 100ATTON: (697)(1812).		Sequence	,a.,	2	3 6	
PEATURE:		US-09-269-717-16 Sequence 10, Appl US-09-902-540-3884 Sequence 3884, Appl	2404 4 U	. o.	1 61.6	
: ORGANISM: Mycobacterium phage Ms6			тепдси пр	re Match	No. Score	
LENGTH: 2404					Result	Re
SOFTWARE: PatentIn Ver. 2.1		SURMARIES		-		
PRIOR RELING DATE: 197-08-06 PRIOR RILING DATE: 197-08-06		to the score of the result being printed, of the total score distribution.	score greater than or equal to the score and is derived by analysis of the total	derived	score and is	
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APPLICANT: DA COSTA GARCIA, "MAGUETA" APPLICANT: DA SILVA ALVES, PSULO J. APPLICANT: DA INVENTION: DNA INTEGRATION INTO "MYCOBACTE!		/1/ina/5B COMB.seq:* /1/ina/6A COMB.seq:*	cgn2_6/ptodata cgn2_6/ptodata	3 2 1		
RIBEIRO DOS SANTOS-ANES		/1/ina/5A COMB.seg:+	Issued Patents NA:*	89	Database :	Da
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C 44 47.8 4.1 15095 4 US-09-902-540-1077			TY_NUC		Scoring table:	Sc
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40 48.2 4.1 1464 4	,		US-09-855-340B-1		Title:	12.
38 48.6 4.1 807 4 39 48.6 4.1 1137 4	-	0.000				
C 36 48.8 4.1 1059 4 US-09-252-991A-15538		April 15, 2000, 17.20.00 (without alignments)	15, 2005, 17	viridw	Run on:	Ru
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31 49.4 4.2 12849 4 US-09-902-540-563 32 49.2 4.2 1473 4 US-09-902-540-2975		- 2005 compagen near	right (c) 1991	Сору		
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1167 CGCCGTCCCCCGATACTTGTCCACCAACCCTGCGTCGGGCCGCCGGCCTGCCCGTGG 1110 GCACGCCCGAAAACCCTCCGCAACAAATACGG---GTTCCTATCGGGGGGCACTGAA 1055 ACATCGCCCGCTGGGTGAAGGTCATGGAAAACCACCGGGGGGCCG-----CGACGGCAA

497 TGCTGCCCCGGCGAGCCGAAAGAGATGAAGTTCCTGAGCGACCCGGAGATCGGTC

437 CGATCTGCGGCGGCGATCGCGGCGAMACGGATCAGGCTCAACCCGTGCTCTTCGA 377 GOGGTCGTCGGAAGCCGCTGCCAGCGAACACAACTGCCAACTGCCACGGCCTGCTGC 317 TCACCCAGCAGTGGGTCAACGACCTGGAGGCCGGCGTCGGCCCGTGGCCGGAGTCCA 995 TOGGCAACGACATOGAACCCAACCTCGGCGACATCCCCTTGTCGAAGCTCTCCGAAG 257 TCCGCAACCACCTCCTGCCCATACTCGGCCATCTCACCCTTGACGAGCTGGACGGGGC

Length 2404; Indels 51, Ga

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TYPE: D ORGANIS FEATURE	APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF I	RESULT 1 US-09-269-717 Sequence 10: ; Patent No. ; GENERAL INF	444	346	3365432	28 29 30
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                                                                                                                                         Query Match
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LENGTH: 1806
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Patent No. 6833447
                                                                                                                                                                                          OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Mycococcu xanthus Genome
FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                       PEATURE:
NAME/KEY: unsure
LOCATION: (1)...(
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                                                                                                                                                                                                                                                                                                      TYPE: DNA
    1222 ATCTTCGAGGGCACCAACGAAATCAACCGCATGCTCATCACCGGCATGCTCCTCAAGCGC 1281
                                         238 AACTCGGAGGGCAACCGGATCCGCAACCTCCTGCCGATACTCGGCCATCTCACCCTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1610 CTGGTCTGGTTCCGCGGCCTACTCCGCACGATCTGCGGCACACGTACGCGTCGTGGCAGC 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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                                                                                                           Score 57.2; DB 4; Length 1806;
Pred. No. 0.003;
                                                                                       Mismatches 294;
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1642
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INSCO-902-940,139/6

Facent No. 683349

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CTGGGCACGCTGGACGTCTTCACGCCATATGACCCNGCGGCGCTGCG 1748

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hintle Gregory J.
APPLICANT: History J.
APPLICANTT: HISTORY J.
APPL
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APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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LOCATION: (1): (4719)
OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 4719
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                                                                                                                                                                                                                                                                                                           3929 CÁTTGGÁCÁTCÁCCCGCGCGCGCGCGNCGCNÍNCTGGÁGCTGCTGTCAGAGCGGGACCTGT 3988
                                                                                                                                       4049 ANGCGATGCAÓGGCATGAAGGCGCCGAGGTGAAGGCCGTGAAGACGCCGGTGAAGTTCG 4108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/902,540
                                             578 ACTOSCGACCGCTCGTGATGCTGCTGGTGGCGACCGGTCTGAGGTGGGGGTGAGGCGATCG 637
                                                                                                                                                                                                                         518 AAGAGATGAAGTTCCTGAGCGACCCGGAGATCGGTCGGCTTATCACGGCGCTTCCGCCGC 577
                                                                                                                                                                                                                                                                                                                                                                                                     458
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Pred. No. 0.0039;
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                                                                                                                                                                                                                                                                      RESULT 6
US-09-821-167-15
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                                                                                                                                       Patent No. 6569668
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 165;
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PRIOR FILING DATE: 2000-07-10
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APPLICANT: Sizer, Seven C.
APPLICANT: Wispard Mosporus vanthus Genome Sequences and Uses Ther
ITIES OF INVESTIGATION (MOSPORUS VANTHUS GENOME SEQUENCES and Uses The
ITIES OF INVESTIGATION (MOSPORUS VANTHUS CENTRE SERVICE) (1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                         Sequence 15, Application US/09821167
                                             APPLICANT:
                                                                                          APPLICANT: Hosted Jr.,
APPLICANT: Horan, Ann C.
TITLE OF INVENTION: Isolated Nucleic Acids from Micromonospora rosa
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OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Myxococcus xanthus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCTCCAGGAGCTGGCCAGCACGGGAGAGCTCGTCTTCCAGTCGCCG 744
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                                                      Jr., Thomas J.
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0; Score 57; DB 4; Pred. No. 0.0045 D; Mismatches 1

DB 4; Length 11282 182; Indels

Gay

NUMBER OF

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US-09-821-167-
CURRENT APPLICATION NUMBER: US/09/821,167
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/194,461
PRIOR FILING DATE: 2000-04-04
                                                                         APPLICANT; Horsed dr., Thomas J.
APPLICANT; Horsen, Ann C.
TITLE OF INVENTION; Isolated Nucleic Acids from Micromonospora Yosaria
TITLE OF INVENTION; plaemid pMG2 and Vectors Made Therefrom
File REFERENCE; 1901199
                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                     Sequence 1, Application US/09821167
Patent No. 6569668
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CURRENT FILING DATE: 2001.03-29
PRIOR APPLICATION NUMBER. US 60/194,461
RIGHT FILING DATE: 2000.04-04
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Micromonospora rosaria
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                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCTG---CGGCTCGCCGGTÄGCCTCCÄCGCCGTTGACGGTCGTGACCGGGAGATCGCCA 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOGCGGTCACGGATCTGCTGTACGGGACCTGCCGTGACGAGGTCGACGAGGGGATCCTCG 1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGTCGTACCCGTGATCCGCCTGCACCTCGACGAGTTCGCCGGGAAGGATCGCCTGTTCG
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Pred. No. 0.0037;
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                                                                 GENERAL INFORMATION
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                                                                              Sequence 3606, Application US/09902540
Patent No. 6833447
                                       APPLICANT: Goldman,
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APPLICANT: APPLICANT: APPLICANT:

Goldman, Barry S. Hinkle, Gregory J. Slater, Steven C. Wiegand, Roger C.

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Matches
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SEQ ID NO 1
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LOCATION:
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11118 AMGCCCTTTCCGAGCTGGCGGGGCACG 1114
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                                                                                                              1025 TOGOGETCACGGATCTGCTGTACGGGCACCTGCGTGAGGAGGTCGACGAGGGGATCCTCG 1084
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                                    CGGCGATCGAGGAGGCGATGGCCGGCG 1111
                                                                                                                                                        TCGCCGCGCAGACCGGGGCGACCTTGGCCGACCTGATGAAGCGGCTCGGGCACTCGTCCA 11060
                                                                                                                                                                                                                                      GGGGAAAGGTCGGACTCGACACCCTCACCTTCCACGACCTGCGGCACACCGGTCAGACCC 1100
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                                                                                      TGGCTG-
                                                                                                                                                                                             TCCTGATTTCTGCCGGGGGGTCCGCTGTCGGCGATCTCCCGGCCGCCTCGGTCACTCGTCGA 1024
                                                                                                                                                                                                                                                                               GCGAGGAAGCCGGGCTTCCGGGCTTACGCATTCACGATCTGCGGCACACTCACGCGGCGA 964
                                                                                                                                                                                                                                                                                                                    TCAGCCGCGACGGATCACCCCTGCGCGGCGACACCCTGTACCAGGCGTTCGTACGCGCTC 10940
                                                                                                                                                                                                                                                                                                                                                             CCGCGCGAAAGGCGGGATGGTAAGGACGCGCAATTTCCGGGCGGATCTGGGTCAAGGCGT 904
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                                                                     -CGGCTCGCCGGTACCTCCACGCCGTTGACGGTCGTGACCGGGAGATCGCCA 11117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Pred. No. 0.0055;
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CGATCATCATCCAGGGC 6341

GCCGCACTGGCGACCGCTCGTCATGCTGCTGGTGGCGACCGGTCTGAGGTGGGGTGAGC GCCGAMAGAGATGAAGTTCCTGAGCGACCCGGAGATCGGTCGGCTTATCACGGCGCTT

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RESULT 9
US-09-902-540-1173
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LENGTH: 20113
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Patent No. 6833447
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LENGTH: 1329
                                                                                                                                                           Matches 166;
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT, BitAte, Gregory J.
APPLICANT, Start, Stown C.
APPLICANT, Wispand, Boger C.
TITLE OF INVENTION Mycooccus xanthus Genome Sequences and Uses Thereof
PILS REFERENCE: 38-10(15849)B.
                                                                                                                                                                                                                                                                 09-902-540-1173
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1682
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/902,540
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                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Myxococcus xanthus
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PRIOR FILING DATE: 2000-07-10
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CURRENT FILING DATE: 2001-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Myxococcus xanthus
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                                                                                                                                                                                Local Similarity
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                                                     6026 GGGACCGAAGCGGAAGCGCCAACCÁCAGACGGCTGAACACCACCTGCGCCGCGAAGÁT 6085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1113 ACCGCTATAAATCCAGATGCTCACCGCGGACTGCATCAGGTAGTTCGTCAGGGC-CATGC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1173 GACGCAGCAGATGACGACGATGCGCGGCAGCCTTGCCGATGAAGCCCAGGCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1233 GGGACCGANGCGGANGCGCCCAACCACAGACGGCTGAACACCACCTGCGCCGCGAAGAT 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                573
456 CGC---GGCGAAACGGATCAGGCTCAACCCGTGCTCTTCGACGATGCTGCCCCGGCGCGA, 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633 GATCGGCCTGCGCGGCCGGGTCGACCTGCTCGCCGCGCGGGCCCCGGCTGACCGTCGT 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           513 GCCGAAAGAGATGAMGTTCCTGAGCGACCCGGAGATCGGTCGGCTTATCACGGCGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396
                                                                                                396 GGCAGCGAAGACGATCAGCAACTGCCACGGCCTGCTGCACAACGATCTGCGGGCGCGGGGAT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              934 ČGÁTCÁTCATCCAGGGC 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 CGC---GGCGANACGGATCAGGCTCAACCCCTGCTCTTCGACGATGCTGCCCCCGGCGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAGCAGCTCCAGGAGC 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAAGGCCGCCACATATGCCGCGCCCATGGCGGATGTAGCCGGGCTCCTGGAAGCCGTTGA 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGCACTGGCGACCGCTCGTCATGCTGCTGGTGGCGACCGGTCTGAGGTGGGGTGAGGC 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCAGCGAAGACGATCAGCAACTGCCACGGCCTGCTGCACGACGATCTGCGGCGCGGCGAT 455
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.4%;
                                                                                                                                                                                52.4%;
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                                                                                                                                                      Score 53.8; DB 4; Length 20113;
Pred. No. 0.024;
0; Mismatches 147; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53.8; DB 4;
Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 6567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6567, Application US/09902540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 16829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses There FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Myxococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 4.5%;
Local Similarity 44.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6265 CGAAGGCCGCCACATATGCCGCGCCCATGGCGATGTAGCCGGGCTCCTGGAAGCCGTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6205 GCCCCACGGGCGTCAGCACGCCCAGCCAGCGGCTCCAGCGCTCCCGCTGGAAGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6146 ACCCCTATANANTCCAGATGCTCACCGCGGACTGCATCAGGTAGTTCGTCAGGGC-CATC
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                                                                                                                                                      901
688
                                                     961
                                                                                                     628 GCGCGCACGCTGGCGAAGACGATGATTGGCCTGGGCGCGGAGATGGGGAAGAAGATCGT
                                                                                                                                                                                                           568 GACGCGCTGGTGCTGGACGTGAAGGTGGGCAGTGGCGCCTTCATGAAGCGCGACGAGG
                                                                                                                                                                                                                                                           841 TTCACCGCGAMAGGCGGATGGTMAGACGCGCMITTCCGGCGGATCTGGGTCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513
                                                                                                                                                                                                                                                                                                                 508 GTGGACTGCATCCCGCTGATTGCGTCCTCCATCATGAGCAAGAAGCTGGCGGAGGGCAT
                                                                                                                                                                                                                                                                                                                                                                 448 ACGGCGCAGGTGGCCCCGGCGGACAAGAAGCTCTATGCCCTGCGGGACGTGACGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 GGAGAGCTCGTCTTCCAGTCGCCGAAGACCGCGAAGGCCGGCGCACGGTCAGTTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 CIGCCGACGICGGAGIACCGGCGGCGGGTGGCGCGAGGIGAACTGCTGCCTGATTGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 CTGCTCGCCGCGCGGCCGGCTGACCGTCGTCGAGCAGCTCCAGGAGCTGGCCAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 CTGGGGCACACGGGTGGGACCCTGGACAMGCTGGAGTCCATCCCCGGCTTCAACGTCAA
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Conservative

0, Score 52.8; DB Pred. No. 0.023; Mismatches DB 4; 302; Length 879; indels

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US/09/902,540

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GCGTGCGAGGAAGCCGGGCTTCCGGGCTTACGCATTCACGATCTGCGGCACACTCACGC GCGATCCTGATTTCTGCCGGGGGGTCCGCTGTCGGCGATCTCCCGGCCGCCTCGGTCACTC

CCTGCTCACCGACATGGACCAGCCGCTGGGCCGCAAGGTGGGCAACGCGCTGGA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1682
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PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/902,540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wiegand, Roger C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1141 GACGAGGAGCTG 1152
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                                                                1021 TCGATCGCGGTCACGGATCTGCTGCTGCGGCACCTGCGTGAGGAGGTCGACGAGGGGATC 1080
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136 GTCATCGAGGCGGTGGACATGCTCCGCGGCAACGCGCCGGAGGACTACACCGAGGTGACG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   865 CGCGAGAAGGTG 876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                745 GTCATCGAGGCGGTGGACATGCTCCGCGGCAACGCGCCGGAGGACTACACCGAGGTGACG 804
                                                                                                                                                                                                                                                                                                                       901 GCGTGCGAGGAAGCCGGGCTTCCGGGGCTTACGCATTCACGATCTGCGGCACACTCACGCG 960
                                                                                                                                                                                                                                                                                                                                                                                       313 GACGCGCTGGTGCTGGACGTGAAGGTGGGCAGTGGCGCCTTCATGAAGCGCGACGACGAGGAC 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                  841 TTCACCGCGCGAAAGGCGGGATGGTAAGGACGCGCATTTCCGGCGGATCTGGGTCAAG 900
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                                                                                                                                 GC---CCTGCTCACCGACATGGACCAGCCGCTGGGCCGCAAGGTGGGCAACGCGCTGGAG
                                                                                                                                                                                           GOGATCCIGATTTCTGCCGGGGGTCCGCTGTCGGCGATCTCCCCGCCCTCGGTCACTCG 1020
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Slater, Steven C.
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Pred. No. 0.028;
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                                                                                                                                 137
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67 TGGCCGCGGACCGACGAGGCGCCAGCAGCTGGCCGCGAACGCCGAGGAGCTGCAGC 126

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                                                                    Matches 222;
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Lei
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                   Match 4.4%;
Local Similarity 47.1%;
                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,391
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Maki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1141 GACGAGGAGCTG 1152
                                302 AGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGAGGCCGGCGTCGGCCCGT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 CGCGAGAAGGTG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 TATGCCCTCCCGGCGGAGANGCTGGTGGTGGAAGAAGACCGCCCGGTGGAGGAGGAG 17
7 AGCAGCGCCTAGACACCGCCACGCAGCAGCGCGCGGAGCTGGAGGCACGGGTGGCACGGC 66

    Application US/09183861
6365165

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                                                                                                                                                                                                                                                                                                                      (206) 682-6031
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Skeiky, Yasir A.W
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                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                 linear
                                                                                                                                                           Leishmania major
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                                                                                                                                                                                                                                                                                                                                         (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                             David J.
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                                                                                                                                                                                                                                   double
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                                                                    Score 51.4; DB 3; Length 5; Pred. No. 0.042; O; Mismatches 246; Indels
                                                                                                                                                                                                                                                                                                                                                                             210121.420C3
                                                                                                        Length 516;
                                                                    3
                                                                    Gaps
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541 CCGGAGATCGGCTTATCACGGCGCTTCCGCCGCACTGGCGACCGCTCGTCATGCT

COGTGCTCTTCGACGATGCTGCCCCCGGCGCGCGAGCCGAAAGAGATGAAGTTCCTGAGCGA

247 GCCTAGACACCGCCACGCAGCAGCGCGCGAGCTGGAGGCACAGGTGGCACGGCTGGCC 187 CCGCGGACGGCGACGAGGCCCGCCAGCAGCTGGCCGCCGAACGCCGAGGAGCTGCAGCAG 127 AGCGCCTAGACACCGCCACGCAGCAGCGCGGAGCTGGAGGCACGGGTGGCACGGCTG 421 CACOGCCTGCTGCACACGATCTGCGGCGCGGCGATCGCGGCGAAACGGATCAGGCTCAA 362 GGCCGGAGTCCACGCGGGGTCGTCGGGAAGCCGCTGGCAGCGAA-GACGATCAGCAACTC 67 TGGCCGCGGACCGCGACGAGGCGCCCCAGCAGCTGGCCGCGAACGCCGAGGAGCTGCAG 7 AGCAGOSCOTAGACACOSCOACGCAGCAGCGCGCGAGCTGGAGGCACGGGTGGCACGG

CGAACGCCGAGGAGCTGCAGCAGCGCCTAGACACCGCCACGCAGCAGCAGCGCGCGAGCTG

719 CGGGAGAGCTCGTCTTCCAGTCGCCGAAGACCCGCGAAGGGCCGGCGCACGG 769

367 AGGCACGGGTGGCACGGCTGGCCGCGGACCGCGACGAGGCGCCAGCAGCTGGCCGCG 659 ACCTGCTCGCCGCGGGGGCCCGGCTGACCGTCGTCGAGCAGCTCCAGGAGCTGGCCAGC

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302 AGCTGGACGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGAAGGCCGGCGCGTCGGCCCGT 361
                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.4%;
Best Local Similarity 47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                    Matches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER; US/09/551,974N
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NCS: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 650043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/09551974#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 516
                                                                                    127 AGCGCCTAGACACGGCACGCAGCAGCAGCGCGAGCTGGAGGCACGGGTGGCACGGCTGG
                                                                                                                                                                                                                            362 GGCCGGAGTCCACGCGGGGTCGTCGGAAGCCGCTGGCAGCGAA-GACGATCAGCAACTGC
                                                                                                                                                                                                                                                                                                                     302 AGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGAGGCCGGCGTCGGCCCG
                                                                                                                                                                                  67 TGGCCGCGGACCGACGAGGCGCCGAGCAGCTGGCCGCGAACGCCGAGGAGCTGCAGC
                                              CCGTGCTCTTCGACGATGCTGCCCCGGCGCGAGCCGAAAAGAGATGAAGTTCCTGAGCGAC
                                                                                                                                        CACGGCCTGCTGCACACGATCTGCGGCGCGCGCGATCGCGGCGAAACGGATCAGGCTCAAC
                                                                                                                                                                                                                                                                       AGCAGCGCCTAGACACCGCCACGCAGCAGCGCGCGAAGCTGGACGCCACGGTGGCACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 4.0
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Skeiky, Yasir A.W.
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Webb, John R.
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                                                                                                                                                                                                                                                                                                                                                                Score 51.4; DB 4;
Pred. No. 0.042;
0; Mismatches 246;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 516;
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3 Gaps

187 CCGCGGACGGCGACGAGGCCGCCAGCAGCTGGCCGCGAACGCCGAGGAGCTGCAGCAG

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US-09-565-501A-34
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Best Local Similarity 47.18; Pred, No. 0.042;
Matches 222; Conservative 0; Mismatches 246; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Leishmania major
3-09-565-501A-34
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LENGTH: 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6607731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 210121.420C6
CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601 CTOGTOGCGACCGGTCTGAGGTGGGGTGAGGCGAT---CGGCCTGCGCGCGCGGGCCGGGTCG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 GCCTAGACACCGCCACGCAGCAGCGCGCGGAGCTGGAGGCACAGGTGGCACGGCTGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427 ACGCCGAGGAGCTGCAGCAGCGCCTAGACACCGCCACGCAGCAGCGCGCG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               719 CGGGAGAGCTCGTCTTCCAGTCGCCGAAGACCCGCGAAGGGCCCGGCGCACGG 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 AGGCACGGGTGGCACGGCTGGCCGCGGACCGACGACGACGCGCCAGCAGCTGGCCGCGA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541 COGGAGATCOGTCGGCTTATCACGGCGCTTCCGGCGCACCGCTGGTCATGCTG 600
601 CTGGTGGCGACCGGTCTGAGGTGGGGTGAGGCGAT--CGGCCTGCGCGCGGCCGGGCGGGTCG 658
                                                                                                        247 GÉCTAGACACCGECACGEÁGEÁGEGEGEGGAGCTGGAGGCACAGGTGGEACGGETGGEEG
                                                                                                                                                               541 CCGGAGATCGGTCGGCTTATCACGGCGCTTCCGCCGCACTGGCGACGGCTCGTCATGCTG 600
                                                                                                                                                                                                                      187 CCGCGGACGGCGACGAGGCCCGCCAGCAGCTGGCCGCGAACGCCGAGGAGCTGCAGCAGC 246
                                                                                                                                                                                                                                                                        481 CCGTGCTCTTCGACGATGCTGCCCCGGCGGGGGGGGAAAGAGATGAAGTTCCTGAGCGAC 540
                                                                                                                                                                                                                                                                                                                               127 AGCGCCTAGACACCGCCACGCAGCAGCGCGCCGAGCTGGAGGCACGGGTGGCACGGCTGG 186
                                                                                                                                                                                                                                                                                                                                                                                421 CACGGCCTGCTGCACACGATCTGCGGCGCGGCGATCGCGGCGAAACGGATCAGGCTCAAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 GGCCGGAGTCCACGCGGGGTCGTCGGAAGCCGCTGGCAGCGAA-GACGATCAGCAACTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 AGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGAGGCCGGCGTCGGCCCGT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed, Steven G.
Campos-Neto, Antonio
Webb, John R.
Dillion, Davin C.
Skelky, Yasir A.W.
Bhatta, Ajay
Coler, Rhea
Reter Probet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCAGCGCCTAGACACCGCCACGCAGCAGCGCGCCGAGCTGGAGGCACGGGTGGCACGGC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
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           366
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659 ACCTGCTCGCCGCGCGGCCCGGCTGACCGTCGTCGAGCAGCTCCAGGAGCTGGCCAGCA

Search completed: April 15, 2005, 19:15:51 Job time : 252.611 secs

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57.6 171936 57.6 171936 57.6 640681 .1 352938

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8 US-10-425-115-77062 6 US-10-029-386-7651 3 US-10-087-192-1057 8 US-10-322-696-79 US-09-974-300-8405 US-09-974-300-8425 US-09-974-300-6855

Sequence

Sequence 79 Sequence 24, Sequence Sequence

US-09-790-988-1 US-10-424-599-90342 US-09-918-995-13891 US-09-918-995-15222

US-10-025-966A-24

US-10-265-071-24

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 19:01:23; Search time 25.1422 Seconds (without alignments) 8204.076 Million cell updates/sec

Sequence: Perfect score: Title: 4 US-09-855-340B-

Scoring table: Gapop 10.0 , Gapext 1.0 IDENTITY NUC 1 ccccggtacgggttcaattcccatcagtcacccg 34

Total number of hits satisfying chosen parameters: Searched: 5622541 seqs, 3033355566 residues

11245082

987 1723 2239 2749 41936 47115 92219

US-10-052-482-199

Sequence Sequence Sequence Sequence sequence Sequence 854 Sequence 161 Sequence 184

US-10-425-115-132687 US-10-425-115-153346 US-09-814-353-21697 839

16 US-10-287-274-7 9 US-09-070-927A-538 17 US-10-264-237-854 18 US-10-425-115-184239

> Sequence 7, Sequence 538, Sequence 6855 Sequence 8405 Sequence 8425 Sequence 1, A Sequence 770

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Published_Applications_NA:* Listing first 45 summaries

control (product // jubpan/1856 | RRE Will seq. (control (product // jubpan/1856 | RRE cgn2_6/ptodata/2/pubpna/PCT /cgn2_6/ptodata/2/pubpna/US07 NEW PUB. seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Regult No Score 20.6 Match 100.0 5 5 241 5 241 5 315 6 315 6 255 6 255 6 23 Length US-09-855-340-8 US-09-855-340-7 US-10-205-220-1 US-10-767-701-4606 US-10-424-599-116427 US-09-855-340-4 US-09-855-340-5 Sequence Sequence Sequence Sequence Description Sequence 1, Appli Sequence 4606, Ap Sequence 116427, Sequence 1, Sequence Sequence a 6, Appli a 6, Appli a 9, Appli a 4, Appli a 5, Appli a 8, Appli a 8, Appli

C 30 1 25 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2									
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19 55.9 268.1 10 US-09-968-748-59-143.1 19 55.9 268.1 7 US-10-445-59-143.9 19 55.9 268.1 7 US-10-445-144-299-143.1 19 55.9 24316.1 19 US-10-097-122-137-13 19 55.9 24316.1 19 US-10-097-122-137-13 19 55.9 14554.1 19 US-10-097-122-137-13 19 US-10-986-237-23 19 US-10-98	45	2	43	42	41	40	39	38	3/
5.9 1681 10 US-02-948-793-45 5.9 2168 17 US-10-248-59-181 5.9 22168 17 US-10-25-114-296 5.9 22168 13 US-10-087-192-43 5.9 41154 13 US-10-087-192-43 5.9 4154 10 US-10-087-192-187 5.3 300 9 US-09-049-695A-25 5.3 300 19 US-09-049-695A-25 5.3 596 13 US-10-061-690-2				19	19	19	19	19	£.9
1861 10 US-09-08-783-45 1861 10 US-0-482-99-1819 1264 17 US-10-482-111-28 17 US-10-087-192-43 14316 13 US-10-087-92-43 1554 13 US-10-087-92-33 1554 13 US-10-087-92-35 1569 19 US-09-049-658-25 100 19 US-09-668-25 100 19 US-09-668-25 100 19 US-09-668-25	5	5	S	5	5	5	'n	5	9
US-10-948-83-45 US-10-424-599-1819 US-10-425-114-2986 US-10-87-192-43 US-10-087-192-1579 US-09-049-655A-25 US-10-926-217-25 US-10-061-690-2	596	300	300	15	4	2368	2364	1681	TOOL
-09-048-783-45 -09-048-789-1819 -10-425-114-2986 -10-087-192-43 -10-087-192-43 -10-087-192-2579 -10-926-217-25 -10-926-217-25	13	19	9	13	13	17	17	10	
	-10-061	-10-926	09-049-	-10-087-192-15	-10-087-192-43	-10-425-114-2986	-10-424-599-1819	-09-948-783-45	-00-00

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US-09-855-340-3 GENERAL Sequence 3, Application US/09855340 Patent No. US20020076788A1 INFORMATION:

TITLE OF INVENTION: alte-specific integration into Micromonoapace affine or INVENTION: halphitica and Micromonospoca cirbonacea chromore ILB REFERENCE: INVIGENCE AND INVESTIGATION HALPHICAL CONCERN APPLICATION NOMER: UPO/9555,340 CURRENT FILMO UNDER: 2001-65-15 APPLICANT: Hosted, Jr., Thomas J.
APPLICANT: Horan, Ann C.
APPLICANT: Boran, Ann C.
TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africar
TITLE OF INVENTION: pMLP1 integrace and use of integrating function in

CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION UNMBER: 60/204,670
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 9

SEQ ID NO 3 LENGTH: 34 TYPE: DNA SOFTWARE: PatentIn Ver. 2.1

US-09-855-340-3 Query Match Best Local S Similarity 100.0%; Score 34; ilarity 100.0%; Pred. No. 3 Conservative 0; Mismatch 3.1e-05; DB 9; Length 34;

ORGANISM: Micromonospora carbonacea

CCCCGGTACGGGTTCAATTCCCATCAGTCACCCG 34

믕 S

Matches

54;

Mismatches

Inde1s

0;

US-09-855-340-6

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US-09-855-340-4
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                                                                               Sequence 4, Application US/09855340
Patent No. US20020076788A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
                                  APPLICANT: Hosted, Jr., Thomas J. APPLICANT: Horan, Ann C.
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SEQ ID NO 9
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APPLICANT: Horan, Ann C.
TITLE OF INVENTION: Isolation of
TITLE OF INVENTION: Site-specifi
TITLE OF INVENTION: Site-specifi
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Patent No. US20020076788A1
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Best Local
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PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 9
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CURRENT APPLICATION NUMBER: US/09/855,340
CURRENT FILING DATE: 2001-05-15
    TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africana
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CURRENT APPLICATION NUMBER: US/09/855,340
CURRENT FILING DATE: 2001-05-15
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APPLICANT: Horan, Ann C.
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100.0%; Pred. No.
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                Sequence 8,
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CURRENT APPLICATION NUMBER: US/09/855,340
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/204,670
                                                                                              TITLE OF INVENTION:
                                                                                                                                           TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africana TITLE OF INVENTION: pMLP1 integrase and use of integrating function fo
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APPLICANT: Horan,
                                                                               FILE REFERENCE: IN01164K
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US2002007678BA1 Hosted, Jr., Thomas J. Horan, Ann C.

site-specific integration into Micromonospora halophitics and Micromonospora carbonacea chromosome

25;

Conservative

73.5%; Score 25; DB 9; 100.0%; Pred. No. 0.39;

Length 243;

Indels

0

0; Mismatches

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; ORGANISM: Micromonospora carbonacea
US-09-855-340-5
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                                                                                                    SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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Best Local Similarity
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SEQ ID NO 4
                                                                                                                                                    CURRENT APPLICATION WINNER: US/99/855,340
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/204,670
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: pt-Up integrame and use of integrating function for TITLE OF INVENTION: ste-specific integration into Micromospoza TITLE OF INVENTION: halophirica and Micromosopora carbonacea chromosome FILE REFERENCE: 1001164K
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Patent No. US20020076788A1
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hosted, Jr., Thomas J.
APPLICANT: Horan, Ann C.
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TITLE OF INVENTION:
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NUMBER OF SEQ ID NOS: 9
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PRIOR APPLICATION NUMBER: 60/204,670
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                                               TYPE: DNA
                                                                               LENGTH: 243
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100.0%; Pred. No. 0.39;
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US-10-205-220-1
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; ORGANISM: Micromonospora halophytica
US-09-855-340-7
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Publication No. US20030170663A1
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Patent No. US20020076788A1
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                        SEQ ID NO 1
LENGTH: 580073
                                                                                                                                                                                                       FILE REFERENCE: PRI9SIDDI
CURRENT APPLICATION NUMBER: US/10/205,220
CURRENT FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: US 08/545,528
RIOR FILING DATE: 1995-10-19
RIOR FILING DATE: 1995-10-19
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                                                                                                                                                                                                                                                                                                        PEPLICANT: Framer et al.
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome,
TITLE OF INVENTION: Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITILE OF INVENTION: Isolation of Micromonospora carbonacea war africation for ITILE OF INVENTION: publi integrate and use of integrating function for ITILE OF INVENTION: site-specific integration into Micromonospora TITILE OF INVENTION: site-specific integration into Micromonespora circumsesses.
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                                                                    SOFTWARE: Patentin version 3.3
                                                                                            NUMBER OF SEQ ID NOS: 1
                                                                                                               PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 08/488,018
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CURRENT FILING DATE: 2001-05-15
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ORGANISM: Micromonospora halophytica
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TYPE: DNA
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100.0%; Pred. No. 1.1;
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100.0%; Pred. No. 0.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-205-220-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                    PEATURE:
                                                                                                                                                                                                                                                                                TYPE: DNA
```

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ORGANISM: Mycoplasma genitalium
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Query Match 65.9%;
Best Local Similarity 95.8%;
Conservative
0; Mismatches
             Score 22.4;
Pred. No. 13
                          DB 16;
                     Length 580073;
  Indels
0; Gaps
```

445128 GGGTTCAATTCCCATCAGTCGCCC 445151 10 GGGTTCAATTCCCATCAGTCACCC 33

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US-10-767-701-4606/c
; Sequence 4606, Application US/10767701
; Publication No. US20040172684A1
                          GENERAL INFORMATION:
David K.
```

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules AssociaTITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21 (5335)B CURRENT APPLICATION NUMBER: US/10/767,703 APPLICANT: Kovalic, Davis APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei

NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 4606 LENGTH: 623 CURRENT FILING DATE: 2004-01-29 ORGANISM: Sorghum bicolor TYPE: DNA FEATURE:

US-10-767-701-4606 OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS83965_1

62.9%; Score 21.4; Pred. No. 18; DB 18; Length 623;

3 CCGGTACGGGTTCAATTCCCCATCAGTCACCC 33 Conservative Mismatches

Indels

0

Gaps

382 CCCGCACAGGTTCGATTCCCATCCTTCACCC 352

Sequence 116427, Application US/10424599 GENERAL INFORMATION: Publication No. US20040031072A3 APPLICANT: APPLICANT: La Rosa Thomas J APPLICANT: Kovalic David K Zhou Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement APPLICANT: Cao Yongwei FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 116427 OTHER INFORMATION: unsure at all n locations NAME/KEY: unsure ORGANISM: Glycine max LOCATION: (1 LENGTH: 298 (298)

US-10-424-599-116427 OTHER INFORMATION: Clone ID: PAT_MRT3847_76144C.1

Query Match Best Local Similarity Matches 23; Conserv Conservative 60.6%; 0; Mismatches Score 20.6; Pred. No. 3 DB 17; Length 298; Indels

0;

Gaps

CCCCGGTACGGGTTCAATTCCCATCAG

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8
                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_5258C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-90342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-156-761-1
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                     Best Local Similarity
                                               Query Match
                                                                                                                                                                                            SEQ ID NO 90342
LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 90342, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Publication No. US20030119018A1
                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                           APPLICANT: Chou Yihua
APPLICANT: Chou Yongwei
1771LB OF EMERGENICH: Soy Nucleic Acid Molecules and Other Molecules Associated With
1771LB OF EMERGENICS: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUBRENT PAPLICATION NUMBER: U8/10/156,761
CUBRENT FILING BATE: 2002-05-29
PRIOR PAPLICATION NUMBER: UP 2001-204089
PRIOR PAPLICATION NUMBER: U5-2001-272697
PRIOR PAPLICATION NUMBER: UP 2001-272697
PRIOR PAPLICATION DATE: 2001-08-02
NUMBER: OF SED LID NOS: 131199
                                                                                                                                                                                                                                                                                              FILE REFERENCE: 38-21 (53223) B
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI
                                                                                                                                FEATURE:
                                                                                                                                        ORGANISM: Glycine max
                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (4187715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 9025608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6372729 CGGGTTCAAGTCCCGTCACTCACCC 6372705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194
    25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTGGTACCGGTTCAATTCCCAGGAG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.4*,
                 57.6%; Score 19.6; DB 17; Length 329; 73.5%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20.2; DB 15
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15,
9,
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inde1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9025608;
0,
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                       / OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                   Query Match
Best Local Similarity
                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 15222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hyaeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-75
CURRENT APPLICATION NUMBER: US 09/918, 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                         LENGTH: 556
                                                                                                                                                                                                                                  LOCATION: (1).
```

298 GGITTTGGTTCAATTCCCATGAGTCA 273

GGTACGGGTTCAATTCCCATCAGTCA 30

22:

Conservative

57.6%; Score 19.6; 84.6%; Pred. No. 1 0; Mismatches

1.1e+02, DB 10;

Length 556;

Indels

0; Gaps (556)

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US-09-918-995-15222/c
                                                                                                                                                                                                                                                                          US-09-918-995-13891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-918-995-13891/c
Sequence 15222, Application US/09918995 
Publication No. US20030073623A1 
GENERAL INFORMATION:
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 13891
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13891, Application US/09918995
Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OFTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                                                                                                                             OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                               LOCATION: (1).
                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 438
                                                                                                                                                                                                                  Local Similarity 84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 CCCCGGCCCGGGGGGGGATTCCCCTTTGGCACCCG 327
                                                                                                                             313 GGTTTTGGTTCAATTCCCATGAGTCA 288
                                                                                                                                                                                                    22,
                                                                                                                                                               5 GGTACGGGTTCAATTCCCATCAGTCA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCGGTACGGGTTCAATTCCCATCAGTCACCCG 34
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                               (438)
                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                  Score 19.6; DB 10
Pred. No. 1.1e+02
                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                     Length 438;
                                                                                                                                                                                                    Gaps-
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RESIDUT 134

RESIDUT 154

RESIDUT 154

RESIDUT 154

RESIDUT 155

RESID
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Search completed: April 15, 2005, 22:51:32 Job time : 40.1422 secs BURN HAME BURN SHILL

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 17:52:06; Search time 7.19829 Seconds (Statut Alignments) 7728.696 Million cell updates/sec

Scoring table: Perfect score: Title: Sequence: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 1 ccccggtacgggttcaattcccatcagtcacccg 34 US-09-855-340B-3

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79835 636591

US-09-949-016-16121 US-09-949-016-13453 US-09-949-016-12456 US-09-949-016-15367 US-09-548-938A-1 US-09-548-938A-9 US-09-949-016-13388 US-09-949-016-11808 US-09-949-016-12111 US-09-949-016-16135 US-09-949-016-15238 US-09-386-816C-1 US-10-320-176-1 US-09-088-337B-23 PCT-US93-11153-23 US-09-489-039A-359 US-09-299-843A-23

Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence sequence Sequence Sequence Sequence sequence

ALIGNMENTS

79835 187848 143644 17657

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Sequence Sequence

Total number of hits satisfying chosen parameters: Searched: 1202784 segs, 818138359 residues 2405568

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:*
1 /cgm2 6/prodate/1/ins/5A COMB.seq:*
2 /cgm2 6/prodate/1/ins/5E COMB.seq:*
3 /cgm2 6/prodate/1/ins/6A COMB.seq:*
4 /cgm2 6/prodate/1/ins/6B COMB.seq:* /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to him we a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

TOO, 0	antianhae	00-09-302-340-100		TO/T	01.Z	20.0		
	2000000	10 00 000 000			2	9 1	, 1	
1. App	Seguence 1, App.	US-08-545-528D-1	4	580073	65.9	22.4		
			į		-		-	
g	Description	No. Score Match Length DB ID	DB	Length	Match	Score	No.	
					Query		esult	70

CENERAL INCOMMETION.	; Patent No. 6537773	; Sequence 1, Application	US-08-545-528D-1	KESULI I
		US/08545528D		

TITLE OF INVESTION Nucleotide Sequence of the Mycoplasma Genitalium G Patent No. 6537703 TITLE OF INVESTION: Thereof, and Uses Thereof CURRENT APPLICATION NUMBER: US/08/545,528D CURRENT FILING DATE: 1995-10-19 APPLICANT: Fraser et al

SEQ ID NO 1 PRIOR FILING DATE: 199 NUMBER OF SEQ ID NOS: PRIOR FILING DATE: 1995-06-07 SOFTWARE: PatentIn version 3.1 PRIOR APPLICATION NUMBER: US 08/473,545 PRIOR APPLICATION NUMBER: 1995-06-07 US 08/488,018

US-08-545-528D-1 TYPE: DNA ORGANISM: Mycoplasma genitalium

LENGTH: 580073

Ş Query Match Best Local Matches 23; Similarity Conservative 65.9%; Score 22.4; DB 4; Length 580073; 95.8%; Pred. No. 7.3; 0 Mismatches Indels

0 Gaps

US-09-902-540-180 RESULT 2 Sequence 180, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION: PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10 NUMBER OF SEQ ID NOS: 16825 APPLICAMY: Wiegand, Roger C. TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and FILE REPERENCE: 38-10(15849)B CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10 APPLICANT: APPLICANT: Goldman, Hinkle, Gregory Slater, Steven (Barry S 2001-07-10

Uses There

SEQ ID NO 180

LENGTH:

251 GGGTTCGATTCCCATCGGTCGCCC 228

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US-09-134-000C-892/c
; Sequence 892, Application US/09134000C
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                                                                         Query Match
Best Local Similarity
                                                          Matches
                                                                                                                                                                                                      SEQ ID NO 892
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn Doucetee-Stamm et al TITLE OF INVENTION: LYNN DEVELOPMENT AND THERAPEUTICS TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6632935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09790988
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-09-902-540-180
                                                                                                                                09-134-000C-892
                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/055,778
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHIGENOBU
                                                                                                                                               ORGANISM: Enterococcus faecalis
                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Buchnera sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP2000-107160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS FILE REFERENCE: 081356/0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                       LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625858 ATGGGTTCANGTCCCATTAGCCACCC 625833
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10 GOGTTCAATTCCCATCAGTCACCC 33
                                                       21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
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                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 ACGGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                        Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WATANABE, HIDEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                         56.5%; Score 19.2;
87.5%; Pred. No. 28
                                                       0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.8,
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                        DB 4;
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                                                       <u>ب</u>
                                                                                        Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 640681
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                                                       Indels
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Sequence 975, Application US/09902540
Patent No. 6833447
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US-09-902-540-975
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                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9122
LENGTH: 1203
                                                                                                                                                      Matches 24,
                                                                                                                                                                         Best Local
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hinkle, Gregory J.
APPLICANT: Miegra, Seven C.
APPLICANT: Miegand, Roger C.
APPLICANT: Miegand, Roger C.
TITLE CF INVESTIGN: Myzococcus xanthus Genome Sequences and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9122, Application US/09902540
Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09711164
Patent No. 6589738
                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US/O:
CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-711-164-7
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                         1098 CCGGTAGAGGTTGAAGCGCCAGCGGTCACCCG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640 CNGGGTCAGGGTTCAATTACCATCGGTAAATCG
                                                                                                            3 CCGGTACGGGTTCAATTCCCATCAGTCACCCG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24,
                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Forsyth,
                                                                                                                                                      Conservative
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72.7%;
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                                                                                                                                                                  Score 19.2;
Pred. No. 41;
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Pred. No. 37
                                                                                                                                                  Mismatches
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                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        672
                                                                                                                                                  8,
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                                                                                                                                                                                     Length 1203;
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GENERAL INFORMATION

a complete of

Gaps

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US-08-815-175-2
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US-09-902-540-975
LIBRARY: PANCTU
CLONE: 2235738
-08-815-175-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Misgand, Roger C.
TITLE OF INVESTION: Myococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)8
                                                                                                                                                                INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/217,883
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CURRENT FILING DATE: 2001-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                      TOPOLOGY: line
IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 10276
                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0225 US
                                                                                       STRANDEDNESS: single
                                                                                                                                                                                  TELEPAX:
                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
FILING DATE: Filed
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                  nucleic acid
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Hinkle, Gregory J.
Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                               415-845-4166
                                        PANCTUTO2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sn
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                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sod
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US-09-573-080A-42

DATABASE ENTRY DATE: 1996-01-26

DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)

Macches Query Match Best Local Similarity

23;

Conservative

0, Mismatches Pred. No. 8

55.3%; 76.7%;

DB 4,

Length 3037;

Indels

0; Gaps

US-09-221-017B-256/c RESULT 10

1713 CCCCGAGAGGGGGGTCAAGTCCAATCTGTCA 168

1 CCCCGGTACGGGTTCAATTCCCATCAGTCA 30

Sequence 256, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION:

APPLICANT: Ross, Bruce C

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120

ZIP: 94304-1018 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

COUNTRY:

STREET: /--CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

755 PAGE MILL ROAD USA

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US-09-573-080A-42/c
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Best Local Similarity 69.7%;
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NUMBER OF SEQ ID NOS: 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
DATE: 1992-10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KBY: misc_feature
OTHER INFORMATION: n is a, c, g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: hervl68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497 CCCCAGTAGGGNTTCAGGGGCCATNAGTGNCCC 529
                                            286-291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOAN, KNOLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROGAN, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn version 3.0
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Pred. No. 5
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IBM Compatible

Windows

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US-07-925-695-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                              sequence 6, Application US/07925695
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 256:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                              APPLICANT: OKAMOTO, I
APPLICANT: NAKAMURA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: POR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F
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APPLICATION NUMBER:
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                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                               TITLE OF INVENTION:
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Local Similarity 76.7%;
                                                                                                                                                                                                                             ITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_teature
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REGISTRATION NUMBER: 32,430
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                                                                      COUNTRY:
                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                     2051 CGGTACATATTCGTTTACCATCAGTCGCCC 2022
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                                                                                                     Washington
                                                                                       D.C
                                                                                                                                                                                          INVENTION:
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                                                                                                                       1850 M Street, N.W., Suite 800
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                                                                                                                                                                                                                                                            OKAMOTO, Hiroaki
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                                                                                                                                        Beveridge, DeGrandi, Weilacher & Young
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                                                                                                                                                                                             DETECTION SYSTEMS
                                                                                                                                                                                                           POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND
                                                                                                                                                                                                                                NON-A, NON-B HEPATITIS VIRUS GENOME
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Pred. No. 99;
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US-07-925-695-7
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Best Local Similarity 66.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/07925695
Patent No. 5428145
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OKAMOTO, Hiroak
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                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 199208
                                                                                                                                                                                                                                                                                                                                                CITY: Washington
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                  FILING DATE:
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                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Weilacher, Robert G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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1850 M Street, N.W., Suite 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DETECTION SYSTEMS
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 Mismatches

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NAME: Weilacher, Robert G. REGISTRATION NUMBER: 20,531

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25 ; Lambel 2463; 9; Indels 0; Gaps 0 Gaps 0 Gaps 0 Gaps		Query Matches Matches Matches 233 SULT 15 -08-587-38 Sequence 1 Sequence 1 GENERAL IN GE	MANE: OLTF: JAMES A REGISTRATOR NUMBER: REGIST	APELICANT, MCCHIAN, RI TITLE OF INVESTIGATION, RICCOGULANT POLYPETIDES TITLE OF INVESTIGATION, ATTOCOMERS. COMMENS AND ENGINEERS. ADDRESSED, COLIFF 6 MESSIGNE ADDRESSED, COLIFF 6 MESSIGNE ADDRESSED, ADDRESSED, COLIFF 6 MESSIGNE ADDRESSED, A

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DLIFF & BERRIDGE
BOX 19928 .
WDRIA
                                                                                                                                                                                                             HIDA, BI
TION: ANTICOAGULANT POLYPEPTIDES
SNCES: 27
TENTIN Release #1.0, Version #1.25
TION DATA:
UMBER: US/08/307,444A
19-SEP-1994
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GOTPMARE: PREMETT RELEASE #1.0. Version #1.25

COMMENT APPLICATION DATA

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